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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1 AR100763 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE BASE COUNT ORRIGIN		esult of the control
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mesotheliomas, and
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Submitted (09-NOV-1995) Kai Chang, Laboratory of Molecular Submitted (19-NOV-1995) Kai Chang, Laboratory of Molecular National Cancer Institute, Building 37, Room 4B19, 37 Converse, MSC4255, Bethesda, MD MD20892-4255, USA
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LPAALACWGYWGSLLSEADVRALGGLACDLPGRFVABSSAEVLLDERLYSCPGPLDQDQ
EARAAALQGGGPYGPSTWSVSTMADALRGLLPVLGQPIIRSIPQGIVAAWRORSSRD
EARRAALQGGGPYGPSTWSVSTMADALRGLLDESLLFYKKWELEACVDAALLATQM
PSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLLFYKKWELEACVDAALLATQM
                                                               /translation="malQRLDPCWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTESA
PLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCL
                                                                                                                                                                              carcinoma
                                                                                             /product="mesothelin or
/protein_id="AAC50348.1"
/db_xref="GI:1145724"
                                                                                                                                                                                            /cell_type="HeLa"
/tissue tunc:"
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/chromosome="16"
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                                                                                                       CCCCAGGACCTGGACACGTGTGACCCAAGGCAGCTGGACGTCCTCTATCCCAAGGCCCGC
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        ACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCAGAAA
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ACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCAGAAA
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PD 16-AUG-1994

PF 25-CCT-1993 JP 1993288617

PR 23-CCT-1992 JP 92P 286153

09-DEC-1992 JP 92P 329546

YAMAGUCHI MARE, KOJIMA TET
                                                                                                                                                                                                              Yamaguchi,M., Kojina,T., Oo@da,M. and Ha GENE CODING MAGAKARYOCYTE AMPLIFIER Patent: JP 1994/225767-A 1 15-AUG-1994; CHUGAI PHARMACEUT CO LTD OS Homo sapiens (human) PN JP 1994/25767-A/1 PD 16-AUG-1994 JP 1993288517 PF 25-OCT-1993 JP 1993288517
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E07943.1 GI:21760
JP 1994225767-A/1.
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PC C12N15/16,C12N1/21,C12N5/10,C12P21/02//A61K37/02,C07K13/00, PC
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2129)
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Homo sapiens
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C (C12N1/21,C12R1:19),(C12N5/10,C12R1:91),(C12P21/02,C12R1:19),

C (C12P21/02,

C (C12R1:91);
        5'UTR
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                                                                                    anti-sense:
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hypothetical: No;
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       /organism='Homo sapiens'
/cell_line='HPC-Y5'
/clone='pKP027'
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                                                                            Location/Qualifiers
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                                                                         CTTGCGACCTGCCTGGGCGCTTTGTGGCCGAGTCGGCCGAAGTGCTGCTACCCCGGCTGG
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                                GCTGGGGTGTGCGGGGGTCTCTGCTGAGCGAGGCTGATGTGCGGGCCTCTGGGAGGCCCTGG
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/db_xref="taxon:9606"
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1918	Qy 1859 GCATCCCCAACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTGGGGGACGC Dh 1838 GCATCCCCAACGGCTACCTCTTACACCTTCTAAACGTCAAAAGACTCCTCTCTCAGACGTCTCTCTC	
1858 1837	Qy 1799 ACTGGATCCTACGGCAGCGGCAGGACGACCTGGACACGCTGGGGCTGGGGCTACAGGGCG	
1798 1777	Qy 1739 AACTTCTGGGACCCCACGTGGAGGCCTGAAGGCGGAGGAGGAGCGGCACCGCCCGGTGCGGG	
1738 1717	Qy 1679 CCACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCAGA	
1678 1657	Qy 1619 GTGGGGCCCCACGGAGGATTTGAAGGCCCTCAGTCAGCAGAATGTGAGCATGGACTTGG	
1618 1597	155 153	
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1378 1357	319 CTCAGGCTCCTCGGCGGCC	
1318 1321	59 TGACGTCCCTGGAGACCCTGAAGGCTTTGCTTG 	
1258 1261	Qy 1199 TCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGTGGAATG	
1198 1201	13	
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901	839 GGGCCTGCTGCCCGTGCT	
841	Db. 782 GCGGGGGACCCCCCTACGGCCCCCCGTCGACATGGTCTGTCT	

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1838 GCATCCCCAACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGGCCCTCTCGGGGACGC 1897

Ouery Match Best Local Similarity 97.0%; Pred. No. 0; Matches 2075; Conservative 0; Mismatches 35; Indels 30; Gaps 3; Qy 5 ATTCCGGCACGGCCACTCCCCTTCGTGTGACGGGGACAGAGCTACCGGTGGAC 64	RESULT 5 189985 189985 189985 189985 189985 DEFINITION Sequence 34 from patent US 5723318. ACCESSION 189985.1 GI:3409925 KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. 1 (bases 1 to 2129) AUTHORS Yamaguchi, N., Kojima, T., Oh-eda, M. and Hattori, K. TITLE DAA coding for megakaryocyte potentiator FEATURES SOURCE 1. 1. 2129 BASE COUNT 389 a 716 c 657 g 367 t	Qy 1919 CCTGCCTCCTAGGACCTGGACCTGTTCTCACCGTCCTGGCACTGCTCCTAGCCTCCACCC 1978
Qy 1019 GCGAGATAGACGAGAGCCTCACTTTTCTACAAGAAGTGGAAGCCTGGATGGA	OY 719 TGAGCTGCCCGGGACCCCTGGACCAGGACCAGGAGGCAGGC	Db 422 CTGAGCCCCCGAGGACCTGGACGCCTCCCATTGGACCTGCTGCTATTCCTCAACCCAG 481 Qy 479 ATGCGTTCTCGGGGCCCCCAGGCCTGCACCAGTTCTTCTCCCGCATCACGAAGGCCAATG 538

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REFERENCE
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                                                                                                                                                                                  Submitted (20-FEB-2001) Nat
Gene Collection (MGC), Cance
Institute, 31 Center Drive,
Steven Jones, Jennifer Asano, Ian
Susanna Chan, Readman Chiu, Chris
Letticia Hsiao, Martin Krzywinski,
                                                                     CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. CO DNA Sequencing by: Genome Sequence Centre,
                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                         BC Cancer Agency, Vancouver, info@bcgsc.bc.ca
                                                                                                                                                                                                                                               Strausberg, R.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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s Fjell, Erin Gar
i, Reta Kutsche,
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                                                                                    Consortium (LLNL)
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                          Yaron Butterfield
          Garland, Ran
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National Cancer
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BASE CC
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Matches 2071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ness, Pawan Pandoh, Anna-Liisa Prabbu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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ALSOQNVSMDLATFMKLHTDAVALPLTVARVQKLLGPHVEGLKAEERHRPVBDWILKQR
QDDLDTLGLGLQGGIPKSYLVLDLSVYQEALSGTPCLLGPGPVLTVLALLLASTLA"
823 c 755 g 424 t
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DPSWRQPERTILPPRFREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQ
MDRVWAAIPFTYEQLLVYLKHKLDELYPDGYPESSYIOHLGYLFLKWSPEDIRKWNYTSLE
TLKALLEYNKGHEMSPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSS
                                                                                                                                                                                                                                                                                                                                     /translation="MALPTARPLIGSCGTPALGSLLFLLFSLGWVQPSRTLAGETGQA
APLDGVLANPPNISSLSPRQLLGFPCAEVSGLSTENELAVALAGKNVKLSTEGLRC
LAHRUSEPPEDLDALFLDLLLFLNDDAFSGPQACTRFFSRLTYKANVDLLFRGAPERGA
LLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQ
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/db_xref="LocusID:10232"
/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_39"
/lab_host="DH10B-R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="mesothelin"
/protein_id="AAH03512
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                           Score 1981.8;
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                                                      TGCGGAGGTGTCCGGGCCTGAGCACGGAGCGTGTCCGGGAGCTGGCCTGTGGCCACA
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Kojima, T.
Kojima,T.
Direct Submission
Submitted (23-FEB-1995) to the DDBJ/EMBL/GenBank databases.
Kojima, Chugai Pharmaceutical Co.Ltd., Fuji Gotemba Researc.
Laboratories; 1-135 Komakado, Gotemba-shi, Shizuoka prefect
                                                                   Unpublished
3 (bases 1
                                                                                                                                                                   and Yamaguchi, N. Molecular cloning and
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/cell_type="pancreatic canc./clone="pKPO27"
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QQEAARAALQGGGPPYGPPSTWSVSTWDALRGLLPVLGOPI IRSIPGGI VAAWRQRSS
RDPSWRQPERTI LRPRFRREVEKTACPSGKKAREIDESLI FYKKWELEACVDAALLAT
QMDRVNAI PFTYEQLLVLKHKLDELYPGGYPESV IQHLGYLFILKMSPEDIRKWNVTSL
ETLKALLEVNKGHEMSPQVATLI DRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELS
SYPPSSI WAVRPQDLDTCDPRQLDVLY EKARLAFQNNNGSEYFYKI QSETLGGAPTEDL
KALSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQ
RQDDLDTLGLGLGGGIPNGYLVLDLSVQEALSGTPCLLGPGPVLTVLALLLASTLA*
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/protein_id="BAA08419.1"
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NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
Tissue Procurement: ATCC
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BC009272
BC009272.1
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
                                                                                                                                                                                                                                                                   Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590,
                                                                                                          DNA Sequencing by: National Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                       cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramur
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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Matches 2039
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This clone was selected for full length sequencing becaused the following selection criteria: matched mRNA
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/protein_id="AAH09272.1"
/db_xref="Gi:14024505"
/db_xref="Gi:14026505
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/db_xref="taxon:9606"
/clone="MGC:10273 IMAGE:3957372"
/tissue_type="Placenta, choriocarc
/clone_lib="NNIH_MGC_21"
/lab_host="DH10B-R"
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Scholler, N. Yang, Y. and
Direct Submission
Submitted (26-AUG-1999) T
511, Seattle, WA 98107, U
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Homo sapiens r
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99432267
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Soluble member(s)
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/codon_start=1
/product="mesothelin/megakaryocyte potentiating factor"
/protein_id="AAF01409.1"
/protein_id="AGF01409.1"
/db_xref="GI:6014587"
/translation="VEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATOMDRVN
AIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKAL
                                                                                                                                                           /db_xref="taxon:
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                                                   GGCCTGAAGGCGGAGCGGCACCGCCCGGTGCGGGACTGGATCCTACGGCAGCGGCAG
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IWAVRPQDLDTCDPRQLDVLPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQ
NVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEFHRPVRDMILRQRQDDLD
TLGLGLQGGIPMGYLVLDLSVQGGRGQARAGGRAGGVEVGALSHPSLCRGPLGDALP
PRTWTCSHRPGTAPSLHPGLRAPLPCWPQPCWGSPPGQEQARVIPVPPQENSRSVNGN
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/db_xref="taxon:10090" /tissue_lib="Lung" /tissue_lib="Lung" /tissue_lib="Lung" /tissue_lib="Lung" /tissue_lib="Lung" /tissue_lib="Lung" 1091286 /function="stimulates the megakasryocyte colony forming activity of murine interleukin-3 in mouse bone marrow cell culture" /codon_start=1 /product="megakaryocyte potentiating factor" /protein_id="BAA13077.1" /db_xref="gi=1408517" /db_xref="gi=1408517" /translation="MALPTARFLIGSCGSDICSRSFLLLLSLGWIPRLOTOTTKTSO EATLLHAVNGAADFASLPTGLFLGLTCEEVSDLSMEQAKGLAMAVRQKNITLRGHQLR CLARRLPRHLTDEELNALFLDLLLFLNPAMFPGQQACAHFFSLISKANVDVLPRRSLE	mouse mRNA for megakaryocyte potentiating factor, complete cds. D86370. D86370. GI:1408516 megakaryocyte potentiating factor. mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2135) Kojima, Chugai Research Institute for Molecular Medicine, Inc., Cytokine Research Program; 153-2, Nagal, Nilhari, Ibaraki 300-41, Japan (E-mali:kojimat@mb.infoweb.or.jp, Tel:0298-30-6211, Fax:0298-30-6270) 2 (bases 1 to 2135) Kojima, T., Oh-eda, M., Hattori, K. and Oh-eda, M. mouse Megakaryocyte Potentiating Factor cDNA Unpublished (1996) 3 (sites) Kojima, T., Oh-eda, M., Hattori, K., Taniguchi, Y., Tamura, M., Ochi, N. and Yamaguchi, N. Molecular cloning and expression of megakaryocyte potentiating factor cDNA J. Biol. Chem. 270 (37), 21984-21990 (1995) Uccation/Qualifiers e	CTAGACCTCAGCGTGCA

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14 GACGCCCTGCCTACGACCTGGACCTGTTCTCACCGTCCTGGCACTGCTCCTA	<u> </u>	
854 GGGCGGCATCCCCAACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGAGCCCTCTCGGG	Qy 18	
794 GCGGGACTGGATCCTACGGCAGCGGCAGGACCACGACACGCTGGGGCTGGGGCTACA	Qy 17 Db 17	
734 GCAGAAACTTCTGGGACCCCACGTGGAGGGCCTGAAGGCGGAGGAGGGGCACCGCCCGGT	Qy 17 Db 17	
74 CTTGGCCACGTTCATGAAGCTGCGGACGGATGCGGTGCCGTTGACTGTGGCTGA	Qy 16	
614 CCTGGGTGGGGCCCCCACGGAGGATTTGAAGGCGCTCAGTCAG	Qу 16 Db 16	
554 GGCCGCCTTGCTTTCCAGAACATGAACGGGTCCGAATACTTCGTGAAGATCCAGTCCTT	Oy 15	
494 GGTCAGGCCCCAGGACCTGGACACGTGTGACCCCAAGGCAGCTGGACGTCCTCTATCCCAA	Qy 14	
434 GTACCTGTGCTCCCTCAGCCCCGAGGAGCTGAGCTCCGTGCCCCCCAGCAGCATCTGGGC	Оу 14 Въ 14	
74 GAAGGGAAGGGCCAGCTAGACAAGACACCCTAGACACCCTGACCGCCTTCTACCCTG		
314 GAGTCCTCAGGCTCCTCGGCGGCCCCTCCCACAGGTGGCCACCCTGATCGACCGCTTTGT	Qy 13 Db 13	
254 GAATGTGACGTCCCTGGAGACCCTGAAGGCTTTGCTTGAAGTCGACAAAGGGCACGAAAT	Qy 12 Db 12	
194 TGTGATCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGTG	Qy 11 Db 12	
134 GCAGCTGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAAGGTTACCCCGAGTC	Qy 11 Db 11	
074 GGATGCGGCCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGA	Оу 10 рь 10	
014 GGCCCGCGAGATAGACGAGAGCCTCATCITCTACAAGAAGTGGGAGCTGGAAGCCTGCGT	Qy 10 Db 10	
954 CATCCTCCGGCCGCGTTCCGGCGGGAAGFGGAGAAGACAGGCTGTCCTTCAGGCAAGAA 	Qy s	
894 CGTGGCCGCGTGGCGCCAACGCTCCTCTCGGGACCCATCCTGGCGGCAGCCTGAACGGAC 1	Qy 8	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-AUG-1996) to the DDBJ/EMBL/GenBank database Hino, Cancer Institiute, Department of Experimental Pathc Kami-Ikebukuro 1-37-1, Toshima-ku, Tokyo 170-8455, Japan (E-mail:ohino@ims.u-tokyo.ac.jp, Tel:03-5394-3815,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamashita,Y., Yokoyama,M., Kobayashi,E., Takai,S. and Hi
Mapping and determination of the cDNA sequence of the Er
preferentially expressed in renal cell carcinoma in the
mutant (Eker) rat model
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Mammalia; Eutheria;
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LHAIPSSVMHLVGLHDLDKCSQRHLGILYQKACSAFQNVSGLEYFEXIRTFLGGASRE
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RQQQKDLDSLGLGLQGGIPNGYLILDFNVREAFSSGAPLLGPGFVFAWIPALLSALRL
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91. .1968
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/db_xref="GI:10129878"
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/cell_line="ERC33"
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/note="AluSx repeat: r
1991. .2128
/note="FLAM_C repeat:
2332. .2626
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                                                             1620. .1931
                                                                                                                                                        200
                                                                                           741. .1033
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                           /note="AluJb
                                                                                                        /note="THE1C repeat:
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                                                                                                                                                                                                  /clone_lib="LA16"
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/db_xref="taxon:9606"
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                                                                                                                                   note="Alusq repeat:
                                                                                                                                                                                                                  /clone="LA16-335H7"
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                                                                                                          matches
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requests: clonerequest@sanger.ac.uk

On Apr 22, 2001 this sequence version replaced gi:9798432.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPORTANT: This sequence is not the entire insert of clone LA16-335H7 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone LA16-335H7 is at 1 in this sequence. true left end of clone LA16-321D2 is at 37208 in this sequence. true right end of clone LA16-444G9 is at 6146 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep LA16-335H7 is part of a clone contig from the tip of the short arm of chromoson 16 spanning 2Mb of p13.3 (Higgs D.R., Filnt J., Daniels R., MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxfc (unpublished), and is from the Los Alamos, flow sorted human Chromosome 16 libraries constructed by Norman Doggett (unpublished), VECTOR: sCos-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP attabases can be found at
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Submitted (17-APR-2001) Sanger Centre, Hinxton, Cambri
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
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2638. .2929
                                                                                                                                                                                                       10747. .10844
/note="L1ME2 repeat: matches 5162.
                                                                                                                                            /note="Alux repeat: matches 1. .295 of consensus" 11372. .11499
                                                                                                                                                                            /note="L1ME2 repeat: matches 4946.
11048. .11336
                                                                                                                                                                                                                                                                                                                     /note="L1M4 repeat: matches 5314. .5379 of consensus"
10031. .10076
/note="L1MB8 repeat: matches 6126. .6173 of consensus"
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/note="MER49 repeat: matches 5. .285 of consensus"
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/note="AluSq repeat:
                                                                          note="Alux repeat:
11805. .12112
                                                                                                                                                                                                                                                        10230. .10530
/note="AluSx repeat: matches 1.
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/note="AluJo repeat: matches 2.
9970. .10029
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/note="L1MB4 repeat: matches 5518.
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/note="AluSx repeat: matches 1.
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/note="AluSq repeat:
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/note="MER4D repeat: matches 411. .536 of consensus"
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/note="L1MB4 repeat:
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note="AluSx repeat:
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/note="AluSx repeat:
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/note="MIR ]
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/note="AluY repeat: matches 1.
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note="match: GSS: Em:AQ166427"
                            'note="AluYb8 repeat:
                                                                                                                           'note="Aluyb8 repeat: matches 10. .132 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                      .571. .9678
note="L1M4 repeat:
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note="L1ME2 repeat: matches 5402.
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                                                            'note="AluSx repeat: matches 1.
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note="Aluo repeat: matches 1. .298 of consensus"
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te="L1MA10 repeat: matches 6172. .6252 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8. .8433
te-"AluSq/x repeat: matches 1. .136 of consensus"
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te="AluSx repeat: matches 1. .294 of consensus"
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te="LlMB4 repeat:
                                                                                                              .11803
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                                                                                           matches 2.
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/note="3
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/evidence=not_experimental
20410. .21099
/note="15 copies 46 mer 67% conserved"
20436. .21077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Tandem repeat. Forced join. Restriction digest data (ECORI, HINCII, SACI) suggest 400 bases are missing." complement(16716. .17130) /note="match: GSS: Em:AQ187418" 17850. .18744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMDRVNÄIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFILKMSPEDIRKWNVTSL
ETLKALLEVNNGHEMSSQAPRAPLPQVATLIDRFVKGRQQLDKDTLDTLTAFYPGYLC
SLSPEELSSYPESSIMAVREQOLDTCOPRQLDVLYPKARLAFQNMNGSBYFVKITQSFL
GGAPTEDLKALSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKABERHRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAPLDGVLANPPNI SSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLR
CLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQ
RLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAC37289.1"
/bxref="GI-13751645"
/ranclatto="GI-13751645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13902. .14202
/note="MER54B repeat: matches 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13670. .13756
/note="MIR_repeat: matches 103. .191 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vrdwilrqrqddldtlglglqggipngylvldlsmqealsgtpcllgpgpvltvlali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQEAARAALQGGGFPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSS
RDPSWRQPERTILRPRFKREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Em: D86370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER54B repeat: matches 310. 618 of consensus" join(15579. 15700,1616B. 16211,16577. 16626,1695B. 117582. 17661,17842. 17971,18045. 1823B,18462. 18552,18542. 17982. 17582. 17582. 17582. 17582. 17582. 17582. 17582. 18235,18594. 19172,19270. 19425,9579. 19745,19820. 19947,20311. 20405,21314. 21500,21583. 21800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(15616. .15700,16168. .16211,16577. .16626,16958.
17582. .17661,17842. .17971,18045. .48238,18462. .185
18626. .18725,18994. .19172,19270. .19425,19579. .197
19820. .19947,20311. .20405,21314. .21500,21583. .216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/product="C335H7.1 (mesothelin)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MSLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
.8858. .18989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="MSLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="C335H7.1 (mesoth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: proteins: Tr:Q61468 Tr:Q14859"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="MSLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: cDNAs: Em:U40434 Em:D49441 Em:E07943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MIR repeat: matches 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="MSLN"
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Pred. No. 1.9e-45;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                     Length 37307;
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TITLE
                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21550 GGTGGGCGCTCTGAGTCACCCCTCTCTCTGTAGAGGCCCTCTCGGGGGACGCCCTGCCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1988 GGCCCACTCCCTTGCTGGCCCCAGCCCTGCTGGGGATCCCCGCCTGGCCAGGAGCAGGC
                                                                                                                                                              CE 2 (bases 1 to 154616)

CE 3 (bases 1 to 154616)

RS Birren.B., Linton.L., Nusbaum.C., Lander.E., Abraham.H., Allen.N.,

RS Birren.B., Linton.L., Nusbaum.C., Lander.E., Abraham.H., Allen.N.,

RS Barra,N., Bastien,V., Beda,F.,

Anderson,S., Baldwin,J., Barra,N., Bastien,V., Beda,F.,

Boguslavkiy.L., Boukhgalter,B., Brown,A., Burkett,G.,

Collymore,A., Cooke,P., DeArellano,K., Colangelo,M., Collins,S.,

Collymore,A., Cooke,P., DeArellano,K., Dewat,K., Diaz,J.S.,

Collymore,A., Cooke,P., DeArellano,K., Dewat,K., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Galagan,J., Gardyna,S., Ginde,S., B., Heaford,A., Horton,L.,

Garand-Pietre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,

Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neil,D., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thoman,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

Voung,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 TGCAGACA 2115
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0 TGCAGACA 21797
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                                                   Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on May 28, 2000 this sequence version replaced gi:7651821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 154616)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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AC067772.2 GI:8099942
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                                                                                                                                                     Direct Submission
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ns clone RP11-728H8, WORKING DRAFT SEQUENCE,
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http://ftp.genome.washington.edu/RM/RepeatMasker.html

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NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14572 14671: gap of 100 bp 114672 17477: contig of 2806 bp in le 17478 17577: gap of 100 bp 17578 21206: contig of 3629 bp in le 21207 21306: gap of 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3884 3983: gap of 100 bp 3984 5809: contig of 1826 bp in 5809 contig of 1826 bp in 5810 5909: gap of 100 bp 5910 7395 contig of 1868 bp in 7396 7495: gap of 100 bp in 7396 7494: gap of 100 bp in 9445 9444: gap of 100 bp 111954 12053: gap of 100 bp in 11254 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 12054 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 728_H_8
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Insert size: 152316; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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11157797
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Daniels, R.J., Peden, J.F.,
Tufarelli, C., Kearney, L.,
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Homo sapiens 16915.3 sequence
AE006464 AE005175
AE006464.1 GI:14336700
                                                                                                                                                                                                                                                                                                                  Submitted (07-DEC-2000) MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, John Radcliffe Hospital, Oxford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels,R.J., Peden,J.F., Lloyd,C., Horsley,S.W., Clark,K., Tufarelli,C., Kearney,L., Buckle,V.J., Doggett,N.A., Flint,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Higgs,D.R.
                                                                                                                                                                                                                                                                                                                                                                          Higgs, D.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
immalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 256073)
                                                          /rpt_family="Low_complexity"
<1. .3757</pre>
                   /note="HS356B8"
<1. .4641
                                                                                                                                                                                        /organism="Homo sapiens"
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/chromosome="16"
/organism="Homo
                                                                                                        23/10/2000"
                                                                                                                       note="GC_rich;
                                                                                                                                                                /map="16p13.3"
                                                                                                                                                                                                                                                       L. .25607
                                                                                                                                                                                                                                                                           Location/Qualifiers
sapiens"
                                                                                                                           RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                  Lloyd,C., Horsley,S.W., Clark,K.,
Buckle,V.J., Doggett,N.A., Flint,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- AGAGACCCTCTCGGGGACGCCCTGCCTCC
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2478. .2582
/note="L2; RepeatMackor -----
                                                                                                                                                                                                                                     /rpt_family="SINE/Alu"
complement(13829. .14055)
note="LIMB8; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5174. .5490
/note="Alusx; RepeatMasker
23/10/2000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSx; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="CpG island; JFP1/SOLH"
/evidence=not_experimental
42. 100
      complement(14808. .14991)
/note="AluJb; RepeatMasker predicted
                                                                                                                                                         complement(14418. .14787)
                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="DNA/MER1_type"
complement(11229. .11378)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="SINE/Alu"
complement(10481. .10623)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/cloa="cosmid 366d1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3433
                                                               rpt_family="LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="SINE/Alu"
complement(8662 . .8958)
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/note="Alux; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SOLH"
                                                                                                                        note="L1MB8; RepeatMasker predicted"
                                                                                                                                                                                                                                                                                                                                                          'note="AluJo; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           507. .4804
/note="AluSx; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="FRAM; RepeatMasker
23/10/2000"
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                                                                                                                                                                              rpt_family="LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MER58; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluSg; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family-"LINE/L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="GC_rich; RepeatMasker predicted
3/10/2000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="GC_rich; RepeatMasker predicted
:3/10/2000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658. .39964
note="HS366D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Similar to Unigene cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 26868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92. .265,6182. .6234,2265. .8378,19053. .20523,
.21437,21524. .21707,21851. .22074,23538. .23663,
...23900,24287. .24448,24537. .24766,24841. .25007,
...25277,25575. .26868)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="Low_complexity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .46058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3596)
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                                 /rpt_family="Low_complexity" 34647. .34860
                                                                                                                                                                                                                                     /rpt_family="Low_complexity"
32807. .32836
/note="GC_rich; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Simple_repeat"
17340 .17414
/note="AluJb; RepeatMasker predicted
23/10/2000"
                                                                                                                                                      /rpt_family="Low_complexity"
32937. .33018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="SINE/Alu"
15007. .15301
/note="Alusx; RepeatMasker predicted
/note="(CA)n; RepeatMasker predicted
                                                                                                                                                                                                      NOTE="GC_rich; RepeatMasker predicted:3/10/2000"
                                                                                                                                                                                                                                                                                                                                                                                                                'note="CpG island; i+E69ncorporates tandem repeat; RJD1"
'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JVILSQLEGNAGESITHRLAHRKAAQAFLSDWTASKGTHSPPLTPEVAGLHGPRPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ?EAGPVRTAGLVATEPARGQCEDKDEEEKEEQEEEEGAAEPRGGWACPRCTLHNTPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="matvgewSCVRCTFLNPAGQRQCSICEAPRHKPDLNHILRLSVE
EQKWPCARCTFRNFLGKEACEVCGFTPEPAPGAAFLPVLNGVLPKPPAILGEPKGSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'product="small optic lobes homolog"
'proteln_id="AAK61233.1"
'db_xref="gi.14336701"
'db_xref="MIM:603267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="SOLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15303. .15414
/note="AluJb; RepeatMasker
23/10/2000"
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13538. .23663,23748. .23900,24287. .24448,24537. .24766,
14841. .25007,25099. .25277,25875. .25752)
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'note="(CCTCG)n; RepeatMasker predicted
                                                                                                            note="GC_rich; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9443. .19488
'note="(GGA)n; RepeatMasker
3/10/2000"
                                                                                                                                                                                                                                                                                                                                                       note="G-rich; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="C-rich; RepeatMasker predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="PubMed:9722942"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="SINE/Alu"
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(19075. .20523.212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family="Low_complexity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="Simple_repeat"
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REFERENCE
AUTHORS
                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                          RESULT 15
AC092381/c
                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                ACCESSION
     TITLE
JOURNAL
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240608 GCAGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGACCCCACGTGGAGGGCCTGAA 240667
                                                                                                                                                                                                                                                                                                                                                                                                                                             241088
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Consensus quality: 133810 bases at least Q40 Consensus quality: 145364 bases at least Q20 Consensus quality: 148096 bases at least Q20 Consensus quality: 148096 bases at least Q20 Estimated insert size: 154000; agarose-fp estimation Estimated insert size: 153570; sum-of-contigs estimation Quality coverage: 5.01 in Q20 bases; agarose-fp estimation Quality coverage: 5.03 in Q20 bases; amo-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
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SUMMARIES
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			٠.	n signal"	ce for membrane			ntigen; mesothelioma; therapy; diagnosis; ss.						Human cDNA sequenc Human polynucleoti	CDNA	DNA clone pcek c1.	Nucleotide sequenc	Plasmid pCiseBON f	Vector plasmid pCM Nucleotide sequenc	Vector pshuttle DN	Nucleotide sequenc	Epstein Barr virus	FLGA insert stabil Nucleotide sequenc	Human cancer assoc	HSV-2 strain SB5 C	HSV-2 immediate ea	Epstein Barr Virus Gene encoding Plas	Human genome from Human ORFX ORF2291	Genomic DNA encodi	Human Lon-protease	Human adenosine Al	Meg-Pot fragment. Human gene signatu Human adenosine Al

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/note= "claim
211..954
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Best Local Similarity
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11-NOV-1992;
09-DEC-1992;
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TGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGGCTCACCGGCTCT
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              CCACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCAGA
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                                                                                 GTGGGCCCCCACGGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTGAGCATGGACTTGG
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                                     aagctgcggacggatgcggtgccgttgactgtggctgaggtgcagaaacttctggga
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                                Diagnosing carcinomas, e.g. adenocarcinoma or ovarian carcinomas, detecting reactivity of a molecule (with an antigenic determinant present in a sample) with an antibody specific for a mesothelin re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesothelin; mesothelin related antigen; MRA; malignant condition; differentiation antigen; adenocarcinoma; mesothelioma; ovarian cappancreatic carcinoma; non-small cell lung carcinoma; MRA-2; ss.
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                                        aagctgcggacggatgcggtgccgttgactgtggctgaggtgcagaaacttctggga
                                                                                                                                                                                                             ggctacctcttcctcaagatgagccctgaggacattcgcaagtggaatgtgacgtccctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.8%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 871.4;
Pred. No. 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          These can be used in the diagnosis, treatment and prevention of cancer, optionally by gene therapy or in the form of a vaccine. present sequence is an example of one of these sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999; 99US-0394374.
01-MAY-2000; 2000US-0561778.
15-AUG-2000; 2000US-0640173.
07-SEP-2000; 2000US-0656668
                                                                                                                                                                                                                                                                           1243 ATTCGCAAGTGGAATGTGACGTCCCTGGAGACCCCTGAAGGCTTTGCTTGAAGTCGACAAA 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 396 BP; 77 A; 139 C; 111 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptides associated with ovarian carcinomas, nucleic acids that encode them, useful for the prevention treatment of ovarian cancers \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF94935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2001.
                                                                                                                                                                                                                                                                                                                                      Local Similarity nes 279; Conserv
                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention provides a number of coding sequences and proteins, over-expression of which is associated with ovarian carcinoma/cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                    GACCGCTTTGTGAAGGGAAGGGGCCAGCTAGACAAAGACACCCTAGACACCCCTGACCGCC
                                                                                                                                     GGGCACGAAATGAGTCCTCAGGCTCCTCGGCGGCCCCTCCCACAGGTGGCCACCCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTACCTGGTCCTAGACCTCAGCGTGCAAG
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2001-211395/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggctacctggtcctagacctcagcgtgcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccccacgtggagggcctgaaggcggagqaycggcaccgcccggtgcgggactggatccta
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-US24827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; vaccine; gene therapy; carcinoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
                                                                                                                                                                                                                                                                                                                                                          10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                          Score 219.8; DB 2
Pred. No. 9.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                           caggtggccaccctgatc
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                                                                                                                                                                                                                                                                                                                                                                                             396;
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                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT AAQO3971 ID AAQO3971 ID AAQO3971 ID AAQO3971 OR-IT OR
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                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                Use of the primers given in AAQ77809-10 in fragments given in AAQ63971.
DNA encoding Meg-Pot has potential use in thrombocytopenia and low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1543
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                                                                                                                                                                                                                                                                                    Sequence 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
platelet; amplification; primer; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1423 TTCTACCCTGGGTACCTGTGCTCCCTCAGCCCCGAGGAGCTGAGCTCCGTGCCCCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 51; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mega:karyoctye potentiator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hattori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9410312-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meg-Pot fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ63971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ63971 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164
                          347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 atccccaacggctacctggtcctagacctcagcatgcaagaggcc
                                                                       \vdash
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DB; AAR53991.
                                                                                                                   AACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGCGTGTCCGGGAGC 346
                      TGGCTGTGGCCTTGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGG
                                                                    aactccttggcttcccgtgtgcggaggtgtccggcctgagcacggagcgtgtccgggagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTATCCCAAGGCCCGCCTTGCTTTCCAGAACATGAACGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agcatctgggcggtcaggccccacgacctggacacgctggggctacggctacagggcggc
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197;
                                                                                               Similarity
                                                                                                                                                                 Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kojima
                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92JP-0286153.
92JP-0301387.
92JP-0329546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-JP01540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 3..197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "Meg-Pot fragment"
                                                                                                                                                                                                                                                                                    32 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA; 197
                                                                                                                                                                                                                                                                                                                                has potential use in treatment of low platelet function.
                                                                                                                                                                                                                  9.28;
                                                                                                                                                                                                                                                                                    66 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oh-eda
                                                                                                                                                                                                           Score 197;
                                                                                                                                                                                                                                                                                    59 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ҈Ӡ.
                                                                                                                                                                 Pred. No. 2. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamaguchi N;
                                                                                                                                                                                                                                                                                    40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potential treatment of
                                                                                                                                                                 2.7e-30;
hes 0;
                                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                       PCR resulted
                                                                                                                                                                                                             Length 197;
                                                                                                                                                                    ·Indels
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1082 CCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGAGCAGCTGG 1141

ccctgctggccggccagatggaccttgtgaatgaaattccctttacctacgagcagctca

61

Query Match Best Local Similarity

7.0%;

Score 150.2; Db ..., Pred. No. 4.9e-21; Pred. No. 4.9e-31;

Indels

Gaps

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Length

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Matches

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Conservative

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                         suppressor genes. (I), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many class II tumour suppressor genes (i.e. genes that are not primary targets for tumour initiating mutations). AAH81492-AAH83376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
                                                                                                                                                                                                          This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour
                                                                                                                                                                                                                                                                                                                      Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483415/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
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Sequence
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Grips M, Hellriegel M, S
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                                                                                                                                                                                                                                                                          Page 488; 579pp;
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59 G;
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Sers C;
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RESULT 9
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XX O7-NOV
XX Human;
KW Human;
KW Human;
KW Human;
KW Tumoux
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  Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                              The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic portion of an ovarian carcinoma acid encoding it, useful for the diagnosis, cancer, preferably ovarian cancer -
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17-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 182; 299pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ovarian carcinoma antigen polynucleotide SEQ ID NO:339
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     Conservative
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99US-0338933.
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87.5%;
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  Score 130.8; DB Pred. No. 3.4e-170; Mismatches 2
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                                                                                                                                  Τ;
                                                                                                                                  11 other;
                                                   DB 21;
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     Indels
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                                           A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-c untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1121
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                                                                                                                                                                                                                                                                                                                                           Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                               Claim 1; Page 1902; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1995
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                                 recognising different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsubara K,
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Sequence

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Η. N other;

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RESULT 11
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XX AAO639
XX Megasa
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KW Platel
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XX HOMO S
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Best Local
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11-NOV-1992;
09-DEC-1992;
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platelet; amplification; primer; polymerase chain reaction;
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                                                                                                                                                                                                                                                                                Sequence 75
                                                                                                                                                                                                                                                                                                                                Use of the primers given in AAQ77805-08 in PCR resulted fragments given in AAQ63969-70.
DNA encoding Meg-Pot has potential use in treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 50; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                New mega:karyoctye potentiator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-167467/20.
P-PSDB; AAR53990.
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                                                    ccagatgcgttctcg
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                                                                                                                                                                                                                                                                              BP; 11 A; 31 C; 16 G; 17 T; 0 other;
                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92JP-0286153.
92JP-0301387.
92JP-0329546.
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                                                                                                                                                                                                           3.5%;
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                                                                                                                                                                                                                                                                                                              has potential use in treatment of low platelet function.
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Pred. No. 3.6e-09;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         potential treatment of
                                                                                                                                                                                         DB 15; L
2.9e-06;
hes 0;
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                                                                                                                                                                                                                           Length 75
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Best Local Similarity
Matches 69; Conserv
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11-NOV-1992;
09-DEC-1992;
                                                Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of the primers given in AAQ77805-08 in PCR resulted fragments given in AAQ63969-70.
DNA encoding Meg-Pot has potential use in treatment of
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platelet; amplification; primer; polymerase chain reaction;
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                                                                                                                                                           10-OCT-1996 (first entry)
                                                                                                                                                                                                                             AAT25748 standard; cDNA to mRNA; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69 BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 50;
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                                                                                                                        Human gene signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHUS ) CHUGAI SEIYAKU
                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 343 GAGCTGGCT 351
                                                                                                                                                                                                                                                                                                                61 gagctggct 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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92JP-0301387.
92JP-0329546.
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Pred. No. 4.4e-0
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                                                                                      frequency;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AART19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of
                                                                                impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a CDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                             AAX53491 standard; DNA; 114955
                                                                                                                                                                                                                                                                                                                                                                                                   2114 CAAAAAAA 2121
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                                                respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema.
                                                                                                                                   Antisense oligonucleotide; multiple target; antisense treatment
                                                                                                                                                                      Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                        05-JUL-1999 (first entry)
                                                                                                                                                                                                                                            AAX53491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCCCCGTTCCACCCCAAGAGAACTCGCGCTCAGTAAACGGGAACATGCCCCCTGCAGA 2113
                                                                                                                                                                                                                                                                                                                                                                   cacgtaaa 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 21.A; 23 C; 14 G; 9 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93JP-0355504
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No. 0.002;
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hepatic metastasis;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergics, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize head to the loss of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligonucleotides (specifically AAX55180-271) can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directed against at least 2 mRNAs selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 37; 120pp; English.
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17-SEP-1997;
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cgcgccgccggcsnnndnnccgcbçgccbgggcgcgccgccggsnnndnnccgcbggccb
                                                               ACCCCCCATAACATTTCCAGCCTCTCCCCTCGCCAACTCCTTGGCTTCCCCGTGTGCGGAG 312
                                                                                                                          ccggccgsnnndnnccgcbggccbgggcgcgcgcgnnndnnccgcbgggccbggg
                                                                                                                                                                                             GCGAGGACCCTGGCTGGAGAGACAGGGACGGAGTCTGCCCCCCTGGGGGGGAGTCCTGACA 252
                                                                                                                                                                                                                                                     nndnnccgcbggccbgggcgcgcccgccggcnnndnnccgcbggccbgggcgcgccg
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                                                                                                                                                                                                                                                                                                                                                                                cbgggcgcgccgccggccgggcsnnndnnccgcbggccbgggcgcgccgccggccgggsn 104378
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97US-0059160
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                              hepatocellular carcinoma; kidney cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes antisense oligonucleotides (AAX52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and CC non-coding regions of RNAs corresponding to target genes, gene CC initiation codons, genomic flanking regions, intron-exon borders, the CC initiation codons, genomic flanking regions, intron-exon borders, the CC initiation and all segments of RNAs encoding proteins associated with one CC compared from sequences AAX55272-74. These multiple target CC conditions or mixtures. The antisense oligonucleotides (specifically AAX5510-271) can be used for the CC conditions are those associated with impaired respiration and CC conditions are those associated with impaired respiration and CC conditions are those associated with impaired respiration and CC conditions, including lung diseases, pulmonary vasconstriction, including lung diseases, pulmonary vasconstriction, conditions are those associated with impaired respiration and CC inflammation, including lung diseases, pulmonary vasconstriction, conditions are those associated with impaired respiration and CC inflammation, including lung diseases, pulmonary vasconstriction, emphysema, chronic collection, pulmonary disease (CODD), and cancer such as leukenias, CC pulmonary hypertension, pulmonary vasconstriction, emphysema, chronic cobstructive pulmonary disease (CODD), and cancers such as leukenias, CC panceratic cancer, hepatocellular carcinoma, kidney cancer, melanoma, comparation metastases, as well as all types of cancer which may metastase entered to the large of cancers which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of cancer which may metastase entered to the large of can
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17-SEP-1997;
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  TCTCCCGCATCACGAAGGCCAATGTGGACCTGCTCCCGAGGGGGGGCTCCCGAGCGACAGC 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCCCCTCGCCAACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGC 334
                                                           GCCCVNNHNNNSCGGCCCGGCCGCGCGCGCCCVGNNHNNNSCGGCCCGGCCGGCGGCGGCG
                                                                                                                   ACCTGCTGCTATTCCTCAACCCAGATGCGTTCTCGGGGGCCCCAGGCCTGCACCCGTTTCT
                                                                                                                                                                                                                                    TGCGCTGTCTGGCTCACCGGCTCTCTGAGCCCCCGAGGACCTGGACGCCCTCCCATTGG 454
                                                                                                                                                                                                                                                                                                                                                 GTGTCCGGGAGCTGGCTGGCCTTGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGC 394
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105114 CGCCCVGGNNHNNNSCGGCCCGGCCGGCGCCGCCCVGGCNNHNNNSCGGCCCGGCCGG 10505

Search completed: December 7, 2001, 10:44:45 Job time: 2642 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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US-08-253-155A-7
US-09-050-863-2
US-09-130-114-1
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Sequence 17, Appl	Sequence 17, Appl	1,	Sequence 1, Appli	Sequence 3, Appli	u	4	'n	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	1,	Sequence 22, Appl	Sequence 21, Appl	Sequence 7, Appli	Seguence 7, Appli	Sequence 7, Appli

ALIGNMENTS

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/00224
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,156
APPLICATION NUMBER: US 60/010,156
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Releat
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 01-DEC-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chang, Kai TITLE OF INVENTION: Mesothelin, a Differentiation Antigen TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                          MOLECULE TYPE: cDNA FEATURE:
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LENGTH: 2138 base pair
NAME/KEY:
LOCATION:
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STATE: California
                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
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                        GCGTGGCGGCAACGCTCCTCTCGGGACCCATCCTGGCGGCAGCCTGAACGGACCATCCTC
                                                  GGGGGACCCCCTACGGCCCCCCGTCGACATGGTCTGTCTCCACGATGGACGCTCTGCGG
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                                                                                                         Query Match
Best Local Similarity
Matches 2138; Conser
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APPLICATION NUMBER: WO PCT/US97/002:
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,166
FILING DATE: 05-JAN-1996
ATTORNEY/ACENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-2591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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APPLICANT: Chang, Kai
TITLE OF INVENTION: MR
TITLE OF INVENTION: Pro-
TITLE OF INVENTION: An
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: No. 6153430 yet assigned CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/776,271
FILING DATE: 01-DEC-1998
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MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
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                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: singi
TOPOLOGY: linear
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                                   Sequence 34, Application Patent No. 5723318 GENERAL INFORMATION:
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Yamaguchi, No.:
Kojima, Tetsuo
Oh-Eda, Masayosh
                                                        US/08426819A
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FEATURE:

NAME/KEY: misc_feature

LOCATION: 1873

OTHER INFORMATION: /note:

OTHER INFORMATION: pKP02:

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NAME: MUTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,77
REFERENCE/DOCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2129 base pairs
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 2075; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDI
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: pKP027
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                  124 TGTTGGTCCTGTGGGGACCGCCC-----TGGCAGCCTCCTGTTCCTGCTCTTCAGCCTCG
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CITY: Falls Church
STATE: Virginia
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STREET: P.O. Box 747
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                                                GGGGAGTCCTGACAACCCCCCCATAACATTTCCAGCCTCTCCCCTCGCCCAACTCCTTGGCT
                                                                                         CCACGGTGCCTCCCTCGCTGGGATCTACACAGACCATGGCCTTG-CAACGGCTCGACCCC
                                                                                                                       GATGGGTGCATCCCGCGAGGACCCTGGCTGGAGAGACAGGGACGGAGTCTGCCCCCCTGG
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                                      GGAGCAGGCACGGGTGATCCCCGTTCCCACCCCAAGAGAACTCGCGCTCAGTAAACGGGAA
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                                                                         ACTGGATCCTACGGCAGCGCAGGACGACCCTGGACACGCTGGGGCTGGGGCTACAGGGCG
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RESULT 4
US-08-426-819A-32
Sequence 32, Appl
Sequence 32, Appl
Patent No. 57233
GENERAL INFORMAT:
APPLICANT: Ye
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TITLE OF INVEN
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CORRESPONDENCE
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CORRESPONDENCE
ADDRESSEE:
STREET: P.
COUNTRY: Fall
STATE: Vix
COMPUTER READD;
MEDLUM TYPE:
COMPUTER: J Sequence 32, Application Patent No. 5723318 GENERAL INFORMATION: Yamagu APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Codi
TITLE OF INVENTION: Potentiato
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, Ster STREET: P.O. Box 747 CITY: Falls Church STATE: Virginia COUNTRY: USA ZIP: 22040-0747 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d. COMPUTER: IBM PC COMPUTER: Yamaguchi, No. compatible Genes Coding Potentiator Stewart, US/08426819A disk 5723318omi Kolasch for Megakaryocyte Birch

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US-08-426-819A-31
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                                                                                                                                                                                                                                                           Sequence 31, Application US/08426819A Patent No. 5723318
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Best Local :
                                                                                                                                                                                                                                                         Patent No.
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SEQUENCE CHARACTERISTICS:
SEQUENCE 197 base pairs
                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                           APPLICANT: Yamaguchi, No. 57:
APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 234
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                             NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Sto
STREET: P.O. Box 747
                                                                                                                                            TITLE OF INVENTION: Genes Coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr., Gerald
COMPUTER READABLE FORM:
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                                          STREET: P.O. Box 7.
CITY: Falls Church
STATE: Virginia
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
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SOFTWARE: Patentl
                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCTGTGGCCTTGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                    CTCACCGGCTCTCTGAGCCCCCCGAGGACCTGGACGCCCTCCCATTGGACCTGCTGCTAT 180
                22040-0747
                                                                                                                                                                                                                        Yamaguchi, No. 5723318omi
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                                                                                                                                                         Genes Coding for Megakaryocyte
                                                                                              Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- fragment
/note- "amplified product from pool D using primers 3AS1 and 7SA1"
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; Pred. No. 6.7e-34;
0; Mismatches 0;
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Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genes Codin TITLE OF INVENTION: Potentiator
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ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                      STRIEST: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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              REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
                                                                                APPLICATION NUMBER: US/08/426,819A FILING DATE: 21-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 21-AP
                                                                                                                                                                                                                                           ZIP: 22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28,977
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Oh-Eda, Masayoshi
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M PC compatible
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; Pred. No. 7.2e-08;
; rematches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 for Megakaryocyte
                                                                                                                                                       Version #1.30
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TELEFAX:

703-205-8050

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US-08-253-155A-7
; Sequence 7, Application US/08253155A
; Patent No. 5691147
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Best Local Similarity 100.0%;
Matches 69; Conservative
                                                           Query Match
Best Local
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SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
                                                                                                                                                                                                                               TELEFAX: (617) 227-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: not
MOLECULE TYPE:
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTIWARE: ASCII(text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/253,155A FILING DATE: 02-JUN-1994
                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE 6 COCKFIELD
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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              945 TGAACGGACCATCCTCCGGCCGCGGTTCCGGCGGGAAGTGGAGAAGACAGCCTGTCCTTC 1004
                                             y Match 2.5%;
Local Similarity 46.4%;
hes 170; Conservative
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CITY: Boston
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                                                                                                                                                                                                                                                                                                            NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
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0; Mismatches
                                             0;
                                           Score 52.4; DB 1;
Pred. No. 0.013;
0; Mismatches 196;
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US-09-050-863-2
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                                                                                                         TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Silva, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammal:
TITLE OF INVENTION: System
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                         MOLECULE TYPE:
                                      STRANDEDNESS:
TOPOLOGY: un
                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                TELEPHONE:
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                                                                                    nucleic acid
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                                             unknown
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                                                                                                                                                                                                  (415) 781-1989
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Query Match Best Local Similarity

2.2%;

Score 46.4; Pred. No. 0.

DB 3;

Length 2580;

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US-09-130-114-1
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                                                                                                  Sequence 1, Application US/08910647 Patent No. 6251433 GENERAL INFORMATION:
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Best Local Similarity 50.4
Matches 113; Conservative
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APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 36 SOFTWARE: FastSEQ for Windows Version 3.0
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                                               TITLE OF INVENTION: Compositions and TITLE OF INVENTION: Polynucleotide De
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                     CORRESPONDENCE ADDRESS:
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                                    NUMBER OF SEQUENCES:
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                                                                                    Zuckermann et al.
Chiron Corporation
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US-08-910-647-1
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Best Local Similarity
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                                                                                                                                                                       NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                              1195 GGAGGGGCAGGAGGAGCAGGAGGGGCAGGAGGGGCAGG
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1752 CCACGTGGAGGGCCTGAAGGCGGAGGAGCGGCCACCGCCCGGTGCGGGACTGGATCCTACG
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                                                                                                                                          STREET: 460 Point San Bruno CITY: South San Francisco
                                                                                                           COUNTRY:
                                                                                                                             STATE:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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                                                             360 Kb floppy disk
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUMBER OF SEQUENCES:
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,
                                              CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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               ATTORNEY/AGENT INFORMATION:
                                                                                                                                           OPERATING SYSTEM:
SOFTWARE: patin (
                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 910/371-7168
                                                                                             APPLICATION NUMBER: FILING DATE: 199205
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Dreger, Ginger
                                                                                                                                                                                                                                                             California
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/08087783A Patent No. 5547856 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                          FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35/60
            REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
                                                                                                                                                            CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/884811
                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2729 GGAGGGCAGGAGGGCAGGAGGAGGGGCAGGCAGGCAGG 2772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1752 CCACGTGGAGGGCCTGAAGGCGGAGGGGGCACCGCCCGGTGCGGGACTGGATCCTACG 1811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 417/77168
                                                                                                                                                                                                   FILING DATE: 1. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415/252-9881
                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/087,783A FILING DATE: 13-Jul-1993
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 460 Point San Bru:
CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                             94080
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                        3.5 inch, 1.44 Mb floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L, Paul J., Lokker, HEPATOCYTE GROWTH
                                                                                                                   07/885971
                                                                                                                                                                                                                                                                      (Genentech)
                                          35,600
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

910/371-7168

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US-08-194-088B-15; Sequence 15, Ap
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US-08-194<sub>-</sub>-088B-15
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Best Local Similarity 50.4%;
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,088B
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/884
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GOdOwski, Paul J. Lokker, Nathalie A. Mark, Melanie R TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 09-FEB-1994
                                   STRANDEDNESS:
                                                                          LENGTH:
                                                                                                                                                                       TELEPHONE:
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                                                                          10596 bases
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415/952-9881
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1632 GGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTGAGCATGGACTTGGCCACGTTCATGAA 1691

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Best Local
Query Match 2.2%;
Best Local Similarity 50.4%;
Matches 113; Conservative
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                                                                                                                                                                        TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 77/
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 18-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                           10596 bases
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                                                                                                         linear
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                                                                                                                        single
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                   Score 46.4; DB 2; Pred. No. 0.33;
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Pred. No. 0.33;
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                                   Length 10596;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match Length DB

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e 10381, e 4654, e 4654, e 1372, e 1372, e 3662, e 3662, e 3662, e 3662,	e 182, Pre 182, Pre 182, Pre 51, Pre 6 151, Pre 6 2780, Pre 6 2780	quence 34, App equence 9499, equence 9530, equence 9551, equence 8662, equence 2725, equence 2725, equence 2715, equence 1716, equence 1716, equence 14, App equence 1681, App equence 7769, equence 10196, equence 10196,	24511, 22854, 6105 A

421 ctctctgagcccccgaggacctggacgcctcccattggacctgctgctattcctcaac 475 CCAGATGCGTTCTCGGGGCCCCAGGCCTGCACCCGTTTCTTCTCCCCGCATCACGAAGGCC [Qy 355 GCCTTGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGGCTCACCGG 414	Qy 295 GGCTTCCCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGCGTGTCCGGGAGCTGTG 354	235 CTGGGGGGAGTCCTGACAACCCCCCATAACATTTCCAGCCTCTCCCCTCGCCAACTCCTT	175 CTCGGATGGGTGCATCCCGGAGGACCCTGGCTGGAGAGACAGGGACGGAGTCTGCCCCC	120 CCCCTGTTGGTCCTGTGGGGACCGCCCTGGCAGCCTCCTGTTCCTGCTCTTCAGC	61 GGACCACGGTGCCTCCCTGGGATCTACACAGACCATGGCCTTG-CAACGGCTCGA	Included the conservative of mismatches 25, indexs AGGAATTCCGGTGGCCGGCCACTCCCGTCTGCTGTGACGCGCGGACAGAGAGACTA		; NAME/KBY: misc_feature ; NAME/KBY: misc_feature ; OTHER INFORMATION: Incyte ID No: 346520.3 US-60-324-185-24511	LENGTH: 2125 ; LENGTH: 2125 ; TYPE: DNA ; ORGANISM: Homo sapiens	o.	TITLE OF INVENTION: POLYMOCLECTIDE SEQUENCE DATABASES, AND SINGLE NUCLECTIDE TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY FILE REFERENCE: GX-0019-1 P FILE REFERENCE: GX-0019-1 P	APPLICANT: Morris, MacDonald APPLICANT: Lal, Preeti APPLICANT: Lal, Preeti APPLICANT: Diep, Dinh TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SECTION FOR DATASETS.	RESULT 1 US-60-324-185-24511 ; Sequence 24511, Application US/60324185 ; GENERAL THEOMETICN.	ALIGNMENTS	42 370.4 17.3 441 31 US-09-867-701-2621 Sequence 2621, Ap 43 370.4 17.3 441 53 US-60-207-484-2621 Sequence 2621, Ap 44 365.2 17.1 503 27 US-09-699-998-1770 Sequence 1770, Ap 45 357.8 16.7 442 17 US-09-330-360-151 Sequence 151, App
Db 1501 gtcaggacctggacctggacacgtgtgacccaaggcagctggacgtcctctatcccaag 1560 Oy 1555 GCCCGCCTTGCTTTCCAGAACATGAACGGGTCCGAATACTTCGTGAAGATCCAGTCCTTC 1614	OY 1435 TACCTGTGCCCCCGAGGAGCTCGGTGGCCCCCAGGAGCATCTGGGGG 1494	1375 AAGGGAAGGGCCAGCTAGACAAAGACACCTTAGACGCCTGACCGCCTTAGCCCTGGGCITTCTAGCCCTGGCCTGACCGCCTTAGCCCTGGCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCATGACTAGACAAGAACAACAACAACAACAACAACAACAACAACAAC	1315 AGTCCTCAGGCTCCTCGGCGGCCCCTCCCACAGGTGGCCACCCTGATCGACCGCTTTGTG	OY 1255 AATGTGACGTCCCTGGAGACCCTGAAGGCTTTGCTTGAAGTCGACAAAGGGCACGAAATG 1314	QY 1195 GTGATCCAGCACCTGGGGTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGTGG 1254	Qy 1135 CAGCTGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAAGGTTACCCCGAGTCT 1194	OY 1075 GATGCGGCCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGAG 1134	OY 1015 GCCCGCGAGAGTAGACGAGAGACCTCATCTTCTACAAGAAGTGGGAGCTGGAAGCCTGCGTG 1074	Qy 955 ATCCTCCGGCCGCGGTTCCGGCGGGAAGTGGAGAAGACAGCCTGTCCTTCAGGCAAGAAG 1014	Qy 895 GTGGCCGCGTGGCGGCAACGCTCCTCCGGGACCCATCCTGGCGGCGGAGCCTGAACGGACC 954	OY 835 CTGCGGGGCCTGCTGCCCGTGCTGGGCCAGCCCATCATCCGCAGCATCCCGCAGGGCATC 894	OY 775 CAGGGGGGGGACCCCCCTACGGCCCCCCGTCGACATGGTCTGTCT	Qy 715 CTGGTGAGCTGCCCGGGACCCCTGGACCAGGACCAGCAGGAGGCAGCCAGGGCGGCTCTG 774	Qy 655 CTGGCTTGCGACCTGCCTGGGGGCTTTGTGGCCGAGTCGGCCGAAGTGCTGCTACCCCGG 714	Oy 595 GCCTGCTGGGGGTGTGCGGGGGTCTCTGCTGAGGAGGCTGATGTGCGGGCTCTGGGAAGC 654	Oy 535 AATGTGGACCTGCTCCCGAGGGGGGCTCCCGAGCGACAGCGGCTGCTGCCTGC

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APPLICANT: MOTTIS, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Lal, Preeti
APPLICANT: Lep, Dinh
TITLE OF INVENTION: Method for the Identific
TITLE OF INVENTION: Method for the Identific
TITLE OF INVENTION: Mothod FOR INVENTION: UMBER: US/60/172,360
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOFTWARE: PERL PROGRAM
SEQ ID NO 22854
LENGTH: 2126
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/XEV: MISC foature
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                          GGACCCACGGTGCCTCCCTGGGATCTACACAGACCATGGCCTTG-CAACGGCTCGA 119
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APPLICANT: MOIRIS, MacI APPLICANT: Lal, Preeti APPLICANT: Lal, Preeti APPLICANT: Diep, Dinh TITLE OF INVENTION: Met TITLE OF INVENTION: Pol
                                                                              Sequence 6105, Applic GENERAL INFORMATION:
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; TITLE OF INVENTION: Identified Thereby
; FILE REFERENCE: GX-0015 p
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 6105
; LENGTH: 2126
; TYPE: DNA
; ORGANISM: Homo sapiens
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte

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US-08-426-819-34
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/426,819
                                                                                                                                                                                                                                                             TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                 CLONE:
FEATURE:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genes Codin
TITLE OF INVENTION: Potentiator
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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CLONE: pKP027
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2129 base pair
                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
TELEPHONE: 703-205-8000
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                                                                       FEATURE:
                                          NAME/KEY:
LOCATION:
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CITY: Falls Church
STATE: Virginia
            OTHER INFORMATION: OTHER INFORMATION:
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TOPOLOGY: no
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                                                                                    LOCATION: '
                                                                                                    NAME/KEY:
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1739 AACTTCTGGGACCCCACGTGGAGGCCTGAAGGCGGAGGAGGAGCACACHILLI	Qy Db	9 CTTGCGACCTGGCGGGCGCTTTGTGGCCGAGTCGGCCGAAGTGCTGCTACCCCGGCTGG 718	Qy 6
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	. סלם	9 TGGCACAGAAGAATGTCAAGAGCTCTCAACAGAGCAGCTGCGCTCTCTGGCTCACCGGCTCT 418	Qy 35 Db 36
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259 TO	Qy Db	179 GATGGGTGCATCCCGCGAGGACCCCTGGCTGGAGAGAGACAGGGACGGAGTCTGCCCCCCTGG 238	Оy
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019 GC 022 GC	. Qy	y Match 93.3%; Score 1994; DB 8; Length 2129; Local Similarity 97.0%; Pred. No. 0; hes 2075; Conservative 0; Mismatches 35; Indels 30; Gaps 3;	Query Best Match

1019 GCGAGATAGACGAGAGCCTCATCTTCTCACAGAAGTGGGAGGCTGACCGAGAGACGCTCAACGAAGTGGGAGAGCCTCACAGAAGTGGGAGAGCCTCACAGAAGTGGGAGAGCCTCACAGAAGTGGGAGAGCCTCACAGAAGTGGGAGAGCCTCACAGAAGTGGAACGCCACAGAGCCTGAACGCCACAGAGCCTGAACGCCACAGAGCCTGAACGCCACAGAGCCTGAACGCCACAGAGCCTGAACCCCACAGAGCCTGAACCCCACAGAGCCTGAACCCCACAGAGCCTGAACCCCACAGAGCCTGAACCCCACAGAGCCTGAACCCCACAGGCTAAACCTGGATGAGCCCTCACAGATGAACCCCTGAACCCACAGGCTACCCCTCTCCTCAAGATGAACCCCTGAACCCACAGGCACCCTGAACCCCTGACCCCTCTCCTCAAGATGAACCCCTGAACCACACACA																		
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CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10869

LENGTH: 2433
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Best Local Similarity
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: AND DIAGNOSIS OF
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, MOVEL NUCLEIC ACID MOLI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1168-001
CURRENT APPLICATION NUMBER: US/09/644,868
CURRENT FILING DATE: 2000-08-28
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 10075
SOFTWARE: FastSEQ for Windows Version 4.0
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RESULT 7
US-09-652-123-9530
Sequence 9530, Appl
GENERAL INFORMATIC
FILE REFERENCE:
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CURRENT APPLICATION
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PRIOR FILING DATE
NUMBER OF SEQ ID
SOFTWARE: FastSI
SEQ ID NO 9530
LENGTH: 2289
                              Sequence 9530, Application US/09652123
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOLIZMAN, DOUGLAS A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID ITILE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,12:
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 9530
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FILLE REPERENCE: 1600.1183-001

CURRENT APPLICATION NUMBER: U$/09/652,12;

CURRENT FILING DATE: 2000-08-30

PRIOR APPLICATION NUMBER: 60/151,134

PRIOR FILING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 10475

SOFTWARE: FastSEQ for Windows Version

SEQ ID NO 9551

LENGTH: 2289

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Sequence 9551, Applic
GENERAL INFORMATION:
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ORGANISM: Homo
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TITLE OF INVENTION: NOVEL NU
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-00
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Sequence 11861, Application US/09698010
GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2029-001
CURRENT APPLICATION UNMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION UNMBER: 60/162,358
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11861
LENGTH: 2289
TYPE: DNA
ORGANISM: Homo sapiens
US-09-698-010-11861
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CCTGGAGACCCTGAAGGCTTTGCTTGAAGTCGACAAAGGGCACGAAATGAGTCCTCAGGC
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RESULT 10

US-09-699-998-8662

Sequence 8662, App

GENERAL INFORMATI

APPLICANT: Holt:

APPLICANT: Gear:

TITLE OF INVENTIC

FILE REFERENCE:

FILE REFERENCE: FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: US/99/699,99
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 10905
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 8662
LENGTH: 2289 APPLICANT: Holtzman,
APPLICANT: Gearing, D
TITLE OF INVENTION: N
TITLE OF INVENTION: T Sequence 8662, Appli GENERAL INFORMATION: TYPE: DNA ORGANISM: Homo Holtzman, Application sapiens g, David P.
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                                      GCGGCAACGCTCCTCTCGGGACCCATCCTGGCGGCAGCCTGAACGGACCATCCTCCGGCC
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LENGTH: 2289
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Best Local Similarity
Matches 2053; Conserv
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CURRENT APPLICATION NUMBER: US/09/710,280
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,537
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 2763
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APPLICANT: Gearing, David P.
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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TITLE OF INVENTION: NOVEL NUCLEIC ACID I
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2036-001
CURRENT APPLICATION NUMBER: US/09/710,28:
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 5803
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 4128
LENGTH: 2289
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APPLICANT: Shyjan, Andrew W.
APPLICANT: Stbdal, Hilde
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APPLICANT: Gearing, David P.
APPLICANT: McCarchy, Sean A.
APPLICANT: McCarchy, Sean A.
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID I
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2005-001
CURRENT APPLICATION UNMBER: US/09/710,280
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,255
PRIOR APPLICATION NUMBER: 60/164,255
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4115
SOFTWARE: FastSEQ for Windows Version 4
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; TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Gearing, I
APPLICANT: Holtzman,
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SOFTWARE: FastSEQ for
SEQ ID NO 1716
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Tumor Associated Molecules (TAMS):
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/60/164,285
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 821
LENGTH: 1108
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 1086; Conserv
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Pred. No. 3.6e-155;
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                                                          AGGCGGAGGAGCGCCCCGCCCGGTGCGGGACTGGATCCTACGGCAGCGGCAGGACGACC 1828
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Search completed: December 7, 2001, 10:40:45
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Copyright (c) 1993 - 2000 Comp
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US-09-970-966-126

US-60-325-795-1

US-09-978-927A-16

US-09-815-264-67667

US-09-815-264-2456

US-09-815-264-72673

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US-09-815-264-766673
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PCT-US01-27760-93 US-09-815-264-67258 US-09-815-264-67392 US-09-815-264-677573 US-09-815-264-62252 US-09-815-264-62252 US-09-388-906A-10829 US-09-388-906A-20855 US-09-815-264-682752 US-09-815-264-682752 US-09-815-264-68284 US-09-815-264-82390

ALIGNMENTS

; NAME/KEY: CDS ; LOCATION: (133)...(562) ; NAME/KEY: misc_feature ; LOCATION: (1)...(562) ; OTHER INFORMATION: n = A US-09-828-792-48 Ъ US-09-828-792-48 Sequence 48, Application US/09828792
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa SOFTWARE: FastSEQ for Windows Version 3 SEQ ID NO 48 LENGTH: 562 Query Match Best Local Similarity Matches 487; Conserv CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER: OF SEO 1D NOS: 1102 FEATURE: ORGANISM: Homo sapiens TYPE: DNA 185 TGCATCCCGCGAGGACCCTGGCTGGAGAGACAGGGACGGAGTCTGCCCCCCTGGGGGGGAG 104 224 tgcagccctcgaggaccctggctggagagacagggcaggaggctgcacccctggacggag 71 TGCCTCCCTCGGGATCTACACAGACCATGGCCTTG - CAACGGCTCGACCCCTGTTGG TCCTGTGGGGACCGCCC----TGGCAGCCTCCTGTTCCTGCTCTTCAGCCTCGGATGGG tgcctccctccctgggatctacacagaccatggccttgccaacggctcgacccctgttgg ggteetgtgggaeeeeegeeteggeageeteetgtteetgetetteageeteggatggg Conservative 19.9%; A,T,C Score 425.2; DB Pred. No. 2e-82; 0; Mismatches or ഒ DB 5; 25; from Indels Length 562; 8 Gaps 223 184 163 129 103 283 244 70

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LENGTH: 553

TYPE: DNA
OGRANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
NAME/KEY: misc_feature
LOCATION: (1)...(553)
OTHER INFORMATION: n = A,T,C oz
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US-09-828-792-182
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TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
CURRENT FILLNG DATE: 2001-04-09
RIOR APPLICATION NUMBER: US/09/838,792
CURRENT FILLNG DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
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PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FASTSEQ FOR WINDOWS Version
DEQ ID NO 182
LENGTH: 553
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; FEATURE:
; NAME/KEY: CDS...(442)
; LOCATION: (78)...(442)
; NAME/KEY: misc_feature
; LOCATION: (1)...(442)
; OTHER INFORMATION: n = A
US-09-828-792-151
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CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
PRIOR FILING DATE: 1999-06-11
PRIOR PRICATION NUMBER: 60/090,258
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 151
LENGTH: 442
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Human Fetal Lung Library
TITLE OF INVENTION: Human Fetal Lung Library
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ATTTCCAGCCTCTCCCCTCGCCAACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTG
                                 gctggagagacagggcaggaggctgcacccctggacggagtcctggccaacccacctaac
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Pred. No. 6.3e-68;
0; Mismatches 27;
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CURRENT APPLICATION NUMBER: US/09/970,966
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 126
; SEQ ID NO 126
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-966-126
US-60-325-795-1
; Sequence 1, Application US/60325795
; GENERAL INFORMATION: .
; APPLICANT: Su, Eric W
; APPLICANT: Wang, He
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Best Local Similarity 80.9%;
Matches 279; Conservative
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APPLICANT: Fling, Steven P.
APPLICANT: xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stolk,
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                                                                                                                                                                                                                                John A.
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Pred. No. 3.5e-38;
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LOCATION: (18)..(2306)
OTHER INFORMATION:
US-60-325-795-1
: LOCATION: (1)..(4282)
: OTHER INFORMATION: n = a,c,g,t any unknown or other US-09-778-927A-16
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                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 16
LENGTH: 4282
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09778927A GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 2511
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Best Local Similarity
Matches 157; Conserv
                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/778,927A CURRENT FILING DATE: 2001-02-08 PRIOR APPLICATION NUMBER: IL 134453 PRIOR FILING DATE: 2000-02-09
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CURRENT APPLICATION NUMBER: US/60/325,795
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                              PRIOR FILING DATE: 2000-03-29 NUMBER OF SEQ ID NOS: 81
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TITLE OF INVENTION: NOVEL SECRETED PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: IL135341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                         FEATURE: misc_feature
                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                              TYPE: DNA
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US-09-815-264-67667
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Best Local Similarity 47.58;
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 67667
LENGTH: 19363
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Best Local Similarity 49.5%;
Matches 161; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/702,134 PRIOR FILING DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Genomic Plant Sequences And FILE REFERENCE: 38-21(51237)G CURRENT APPLICATION NUMBER: US/09/815,264 CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/620,392 PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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               17829 gccgacgtgcacgtcgctggtggcgcagcggtggacgccgccgctcgccgccgtgtggcc
                                                                                   17709 catggagagggcgctgcggaggcggtggcgtcggaggcggaggcgggagctggaggg 17768
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                           1668 CATGGACTTGGCCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGC 1727
                                                     1788 CCCGGTGCGGACTGGATCCTACGGCAGCGGCAGGACCTGGACACGCTGGGGGCTGGG 1847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 CCCGGGACCCTGGACCAGGACCAGCAGGAGGCAGCCAGGGCGGCTCTGCAGGGCGGGGG
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Pred. No. 0.12;
0; Mismatches 163
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                                                                                                                                                                                                                                                         Score 52; DB 5; Length 19363; Pred. No. 0.23;
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                        205; Indels
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CURRENT APPLICATION NUMBER: US/05/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 58041
LENGTH: 17466
TYPE: DNA
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US-09-815-264-58041
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Best Local Similarity
Matches 141; Conserv
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TITLE OF INVENTION: Genomic Plant Sequences
FILE REFERENCE: 38-21(51237)G
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11485 CTCGAGGAGACGTTCTCGAGCTCCAGCCTGCTGCAGATGATCTCCATGTCGCC 11433
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                                                                                    11605 GAGCTCGCCGTCGCGTGCCTGCTGAGCGCCCGAGAACGGGCTCTGCATGCTCGGCGTCGCC 11546
                                                                                                                                                                                                                                                                                                                                                                    1627 CCCACGGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTGAGCATGGACTTGGCCACGTTC 1686
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                                     1867 AACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTCGGGGGACGCC 1919
                                                                                                                         1807 CTACGGCAGCGGCAGGACGACCTGGACACGCTGGGGCTACAGGGCGGCATCCCC 1866
                                                                                                                                                                                                              1747 GGACCCCACGTGGAGGGCCTGAAGGCCGAGGAGCGGCACCGCCCGGTGCGGGACTGGATC 1806
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Koshi, Jeffrey M.
Kovalic, David K.
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RESULT 9 US-09-760-446A-2456

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Best Local 9
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                                                                                        APPLICATION NUMBER: 60/232,398
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FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
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FILING DATE: 2000-09-14
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/2
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FILING DATE: 2000-09-08
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APPLICATION NUMBER: 60/249,214
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APPLICATION NUMBER: 60/249,215
FILING DATE: 2000-11-17
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                                                                                                                               gtggccgcacgaggcgggaggctgagagctgaggagcccggcctacagaggggcccgctg 9656
                                                                                                                                                                        GCTTGCGACCTGCCTGGGCGCTTTGTGGCCGAGTCGGCCGAAGTGCTGCTACCCCGGCTG 717
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                                                                                                  US-09-815-264-76667; Sequence 76667, Application US/09815264; GENERAL INFORMATION:
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US-09-815-264-72273
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LENGTH: 17403
TYPE: DNA
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Best Local Similarity
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
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CURRENT FILING DATE: 2001-03-23
                                              APPLICANT:
                                                               APPLICANT:
                                                                                 APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Genomic Plant Sequences FILE REFERENCE: 38-21(51237)G
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                             APPLICANT:
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                                                                                                                                                                                                                   8741 CGCGGACGAGGCAGAGGCGGCGG 8719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9101 CGTCTAGGGGCAGAGGCACTCGGCGGCGCCCGGATCTGAGAGGACCGGCGGCGGCGCGCTTG 9042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 CGGCTCTGGCCTGGGGGTGTGCGGGGGGTCTCTGCTGAGCGAGGCTGATGTGCGGGCTC 646
                                                                                                                                                                                                                                                        947 AACGGACCATCCTCCGGCCGCGG 969
                                                                                                                                                                                                                                                                                            GTGGACGCGCGGAGGTGGTCGCCGCCCAAGCCGCCGCCCTCATGGAGGCGGCGGCGGT 8742
                                                                                                                                                                                                                                                                                                                                 AGGGCATCGTGGCCGCGTGGCGGCAACGCTCCTCTCGGGACCCATCCTGGCGGCAGCCTG 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCGAGGCGGCGGCTGGATCTGAGTGGAGTGGCGGCGGTGCTAGCGGAGGTGGCGGTCA
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Kovalic, David K.
                         Dotson, Stanton B. Koshi, Jeffrey M.
                                                            Cao, Yongwei
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McIninch, James
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Pred. No. 1.2;
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APPLICANT: APPLICANT:

Liu, Jingdong McIninch, James

TITLE APPLICANT:

OF INVENTION: Genomic Plant Sequences And Uses Thereof

PPLICANT:

FILE REFERENCE: 38-21(51237)G

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CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 76673
SEQ ID NO 76673
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                                                                                                                                                 ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(76304)
; OTHER INFORMATION: unsure at all n locations
US-09-815-264-76673
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US-09-815-264-76667
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Best Local Similarity
Matches 115; Conserv
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SEQ ID NO 76667
LENGTH: 50229
TYPE: DNA
                                             Matches
                                                              Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences
FILE REFERENCE: 38-21(51237)G
FILE REFERENCE: 38-21(51237)G
764
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                                                                                                                                                                                                                                                                             TYPE: DNA
1756 GTGGAGGGCCTGAAGGCGGAGGAGCGCCACCGCCCGGTGCGGGACTGGATCCTACGGCAG 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1876 CTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTCGGGGGACGCCCTGCCTCCTAGGACCT 1935
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Kovalic, David K.
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                                             Conservative
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                                                              2.2%;
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Pred. No. 2.6;
0; Mismatches 112;
                                                              Score 47.8;
Pred. No. 3;
                                         .Mismatches 112;
                                                                                  DB 5;
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                                                                                Length 76304;
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: LOCATION: (1)..(9648)
: OTHER INFORMATION: unsure at all n locations
US-09-815-264-80624
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 80624
LENGTH: 9648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.2%;
Best Local Similarity 43.5%;
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Sequence 80624, Application US/09815264
GENERAL INFORMATION:
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TITLE OF INVENTION: Genomic Plant Sequences
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
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5776 tggacgaggcgacgagcgctggacgtgyagtcggagcgcgtcgtgcagcaggcgctgg
                                                1250 AGTGGAATGTGACGTCCCTGGAGACCCTGAAGGCTTTGCTTGAAGTCGACAAAGGGCACG 1309
                                                                                          5716 nnnnnnnnnnnnnnnnnnnnncgcgcgcgccatcgtgaaggacccggccatcctgctcc 5775
                                                                                                                                      1190 AGTCTGTGATCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCA 1249
                                                                                                                                                                                  5656 gcgcgctgccggagggctaccggacgagaytcggggagcgcggcgtgcagcnnnnnnnnn 5715
                                                                                                                                                                                                                            1130 ACGAGCAGCTGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAAGGTTACCCCG 1189
                                                                                                                                                                                                                                                                      5596 gcgcgacggaggcggaggtggtcgacgcgqcgaagctggcgaacgcgcactccttcatca 5655
                                                                                                                                                                                                                                                                                                1070 GCGTGGATGCGGCCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCT 1129
                                                                                                                                                                                                                                                                                                                                                              5536 agcaagagccggcgctgttcgcgacgaccatctacgacaacatcctctacgggaaagacg 5595
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Kovalic, David K.
Liu, Jingdong
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Pred. No. 1.
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US-09-815-264-79254/c

5836 a 5836

Sequence 79254,

Application US/09815264

APPLICANT: Boukharov, Andrey A.

INFORMATION:

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NAME/KEY: unsure
LOCATION: (1)..(49792)
OTHER INFORMATION: unsure at all n locations
US-09-815-264-79254
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                                                                                                                                              Sequence 2, Application US/09249585A
GENERAL INFORMATION:
APPLICANT: HOTILCK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF
FILE REFERENCE: 0867/D905
CURRENT APPLICATION UNMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
                                        NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENCTH: 1926
TYPE: DNA
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Best Local Similarity 53.2%;
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CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
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PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
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TYPE: DNA
ORGANISM: Oryza sativa
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                    ORGANISM: Epstein Barr Virus
FEATURE:
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Kovalic, David K.
Liu, Jingdong
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Best Local Similarity 50.4%;
Matches 113; Conservative
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ALIGNMENTS

VERSION KEYWORDS SOURCE RESULT 1 AL574127/c COMMENT FEATURES REFERENCE ACCESSION DEFINITION LOCUS AUTHORS TITLE ORGANISM JOURNAL source Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France AL574127 1037 bp AL574127 LTI_NFL006_PL2 Email: segref@genoscope.cns.fr, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1037) Homo sapiens EST. AL574127.1 GI:12934032 prime, mRNA sequence. AL574127 numan. /db_xret="taxu::>>>>
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                      AGGGCGGCATCCCCAACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTCGG 1912
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94.5%;
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Pred. No. 1.4e-135;
2; Mismatches 3;
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L1.W.B., Gruber, C., Jessee, J. and Full-length cDNA libraries and no Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Se BP 191 91006 EVRY cedex - France
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Eukaryota; M
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Location/Qualifiers
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//db_xref="taxon:9606"
//clone=lib="LTI_NFL006_PL2"
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//clone_lib="LTI_NFL006_PL2"
//tissue_type="placenta"
//note="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL:
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Full-length cDNA libraries and Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National
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                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 98)
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/tissue_type="placenta"
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was primed with a NotI-oligo(dT) primer. Five prime
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/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
bttp://fillioner.com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/pcd/sites/com/
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923 bp LTI_NFL006_PL2 RNA sequence.

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Contact: Genoscope
Genoscope - Centre National de Sequencage
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1 (bases 1 to 923)
Li,W.B. Gruber.C. Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/Clone="Type="placenta"
/tissue_type="placenta"
/note="vector: pcmySpORT 6; Site_1: NotI; 1st strand cDNA
/note="vector: pcmySpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMySpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockwille, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
57 a 276 c 301 g 176 t 3 others
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AL578453 LTI_NFL006_PL2
prime, mRNA sequence.
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Contact: Genoscope
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1. (bases 1 to 933)
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                               /clone="CSObKOIIYD2]"
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/tissue_type="placenta"
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/note="Vector: pCWVSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
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            968 bp
LTI_NFL006_PL2
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Pred. No. 4.5
             mRNA
Homo
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1. No. 4.5e-118;
4ismatches 16;
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                                                                    CTCAGCCC-CGAGGAGCTGAGCTCCGTGCCCCCCAGCAGCATCTGGGCGGTCAGGCCCCA
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AL577458.1
EST.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
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Full-length cDNA libraries
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 968)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMYSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSOD1086YLD1"
/clone=LYD="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand was primed with a NotI-cligo(dT) primer. Five primer was primed with a NotI-cligo(dT) primer.
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Genoscope - Centre Nationa
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Li.W.B., Gruber.C., Jessee, J. and Polayes, D.

Li.W.B., Gruber.C. Jessee, J. and Polayes, D.
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LTI_NFL006_PL2
a division of Invitrogen 9800 Medical Center Rockville, Maryland 20850, USA Fax : (1) 301 Email : fliang@lifetech.com URL :
                                       /Clone="CSODK002YCO6"
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/tissue_type="placenta"
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/note="Vector: pCMVSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the NotI and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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immalia; Eutheria;
(bases 1 to 965)
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                                                                                                                                                                                                                                                                                                                                                                   a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: http://fulllength.invitrogen.com" 340 c 314 g 171 t 5 others
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/note="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
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/clone_lib="LTI_NFL006_PL2"
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                                                                                                                                                                                                                                                                                                                                                                                              prime, mRNA sequence.
                                                                                                                         segref@genoscope.cns.fr,
              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CLOBAOO4ZGO8"
/clone_lib="LTI_NFLO06_PL2"
/tissue_type="placenta"
                                                                                                       Location/Qualifiers
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                                       GTCGACATGGTCTGTCCCCACGATGGACGCTCCGCGGGGCCTGCTGCCCGTGCTGGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://fulllength.invitrogen.com"
325 c 297 g 158 t
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Pred. No. 1.8e-110;
4; Mismatches 39;
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Best Local Similarity
Matches 713; Conserv
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CCAAGGCAGCTGGACGTCCTCTATCCCAAGGCCCGCCTTGCTTTCCAGAACATGAACGGG
                                                                                                            CTAGACCACCTGNCCGCTTTCTACCTGGGGTACCTGTGCTCCCTCAGCCCCGAGGAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 1048 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 726)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (amplicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                               liver spleen lNFLS library. 1st strand cDNA was with a Pac I - oligo(dT) primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1674301"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_fetal_liver_spleen_lNFLS
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98.2%;
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Pred. No. 5.7e-99;
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Mammalia; Eutheria; Primates
1 (bases 1 to 817)
Li.W.B., Gruber,C., Jessee,J
Full-length cDNA libraries a
Unpublished (2001)
Contact: Genoscope
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prime, mRNA
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  /db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODK002YC06"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6. ~.
                                                                                   seqref@genoscope.cns.fr,
Location/Qualifiers
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2 LTI_NFL006_PL2
mRNA sequence.
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Primates;
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                                          AGCCAGGGCGGCTCTGCAGGGCGGGGGACCCCC
                                                                                  AGTGCTGCTACCCCGGCTGGTGAGCTGCCCGGGACCCTGGACCAGGACCAGCAGGAGGC
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95.0%;
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                                                                                                               GGGTGGGCCCCCACGGAGGATTTGAAGGCCCTCAGTCAGCAGAATGTGAGCATGGACTT 1676
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
Seq.primer: -40UP from Gibco
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to /3/)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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/db_xref="taxon:9606"
/clone="IMAGE:2421584"
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/tissue_type="adenocarcinoma"
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                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                   High quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL www.bio.llnl.gov/bbrp/image/image.html Insert Length: 1518 Std Error: 0.00 Seq primer: -40UP from Gibco
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                                  /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                        /tissue_type="adenocarcinoma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Pan1"
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/db_xref="taxon:9606"
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        Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 799)
NCI-CGAP http://www.n
                                                                                                             AI744747 799 bp mRNA EST 21-JUN-1999 tr14bll.x1 NCI_CGAP_OV23 Home sapiens cDMA clone IMAGE:2218269 similar to TR:Q14859 Q14859 PRE-PRO-MEGAKARYCCYTE POTENTIATING FACTOR PRECURSOR. ;contains MSR1.t2 MSR1 repetitive element ;,
                                                Homo sapiens
                                                                                 AI744747.1
                                                             numan.
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Primates;
       .ncbi.nlm.nih.gov/ncicgap
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CCTGGACACGCTGGGGCTGGGGCTACAGGGCGGCATCCCCAACGGCTACCTGGTCCTAGA
                                                                       GCCACCCTGATCGACCGCTTTGTGAAGGGAAGGGGCCCAGCTAGACAAAGACACCCTAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
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/db_xref="taxon:9606"
/clone="IMAGE:2218269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 poo
/lab_host="DH10B"
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                                                                                                                                                        Human CAK1 antigen
Megakaryoctye pote
Mesothelin related
Soluble mesothelin
                                                                                                                                                                                                                                                                    Description
                                                                Meg-Pot fragment.
Meg-Pot N-terminal
Meg-Pot fragment.
                       Protein sequence
                                                Human
                                                                                                                                   Mesothelin related
glutamicum
                                              leucine-rich
prote
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	ALIGNMENTS					
T. thermophilus DN	AAR13143	12	834		101.5	5
thermosta		13	789	3.1	101.5	44
Mutant thermostabl	AAR23165	13	758		101.5	ü
Human ORFX ORF2135	AAB42371	21	1084		102.5	12
	AAB93780	22	790		102.5	11
seq	AAB95160	22	546		102.5	Ö
	AAB99495	22	2090		103	39
Mutant thermostabl	AAR26476	13	834		103	8
Bovine DNA-depende	AAY17386	20	941		103.5	37
DNA polymerase I h	AAR96203	17	834		103.5	8
Thermus flavus DNA	AAR99542	17	834		103.5	ω̈
рe	AAY53970	21	1857		104	34
Amino acid sequenc	AAW59945	19	836		104.5	ü
 Amino acid sequenc 	AAW59944	19	836		104.5	32
Protein encoded by	AAW59943	19	834		104.5	ï
Thermus thermophil	AAR79149	16	834		104.5	ö
Heat stable DNA po	AAR43998	15	834		104.5	29
Glutamic acid rece	AAR45945	15	1239		105	8
75	AAW13387	18	804	٠	105.5	27
Murine APLP1. Mus	AAR98903	17	653		106.5	8
Arabidopsis thalia	AAG07306	21	337	٠	107	25
A region polyp	AAR44431	14	3567	٠	107.5	24
Rat 5-oxoprolinase	AAW61369	19	1288	•	107.5	23
Non-reducing sacch	AAY85166	21	757	•	107.5	22
Non-reducing sacch	AAY85151	21	756		107.5	21
Arabidopsis thalia	AAG38206	21	340		110.5	0
Arabidopsis thalia	AAG07304	21	349	3.4	111	9
Arabidopsis thalia	AAG07305	21	346	3.4	111	8
5	AAB74635	22	913	ω .5	113.5	7
Human phospholipas	AAB82415	22	913	ა	113.5	9
LA2 prote	\rightarrow	21	913	ω .5	113.5	5
•••	င္သ	15	23	ω .5	114	4
Arabidopsis thalia	N	21	351	ω .5	114.5	ω
	æ	21	349	ω 5	114.5	2

AAW26674 RESULT Cleavage-site CAK1 antigen; mesothelin; tumour specific antigen; mesothelioma; ovarian cancer; squamous cell cancer; therapy; vaccine; diagnosis 11-MAR-1998 (first entry) AAW26674; AAW26674 standard; Protein; 628 05-JAN-1996; 17-JUL-1997. Region Homo sapiens Human CAK1 antigen (mesothelin). 03-JAN-1997; WO9725068-A2. Key (USSH) US DEPT HEALTH & HUMAN SERVICES Peptide Ц 96US-0010166. 97WO-US00224 /note= "putative membrane insertion signal" 292..293 /note= "putative furin processing site" 587..628 Location/Qualifiers 16..32 /note= "hydrophobic tail typical for GPI anchorage"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bearing an antigen comprising at least 10 contiguous amino acids of mesothelin involves: (a) providing a chimeric molecule comprising the effector molecule attached to a targeting molecule that specifically binds to mesothelin; and (b) contacting the tumour with the chimeric molecule such that the chimeric molecule specifically binds to a tumour cell. Also claimed is a method for inhibiting mesothelin expression or activity by contacting mesothelin bearing cells with inhibitory nucleic acids for the mesothelin gene. The methods can be used to detect tumour cells and to inhibit the growth of cells bearing mesothelin. Mesothelin derived antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on mesothelium, mesotheliomas, ovarian cancers and some squamous cell carcinomas. The antiqen has been designated mesothelin. Its amino acid sequence was deduced from a cDNA clone (see AAT91079) isolated from a HeLa cDNA library. A 40 kDa form (KL) of mesothelin that is found on the surface of human ovarian tumour OVCAR-3 cells appears to be derived from the 69 kDa precursor by several processing steps. A claimed method for specifically delivering an effector molecule to a tumour cell specifically delivering an effector molecule to a tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This protein comprises the human CAK1 antigen which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 58-60; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agents for targeting mesothelin, a tumour cell antigen - used for
the detection or inhibition of growth of e.g. mesotheliomas, ovarian
cancers and squamous cell carcipomas
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                                                                                                     LLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEADV
                                  IDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLD
                                                                                                                                                                                                                                                                          STMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKTAC
                                                                                                                                                                                                                                                                                                         ralgglacdlpgrfvaesaevllprlvscpgpldqdqqeaaraalqgggppygppstwsv
                                                                                                                                                                                                                                                                                                                         RALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTWSV
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Best Local
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11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                        DNA encoding the 584 or 248 amino acid produse in treatment of thrombocytopenia and low
                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 52-57; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-167467/20.
N-PSDB; AAQ63972.
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thrombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                                                                                                      Local Similarity hes 601; Conserv
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                                                                                 ETLSGTPCLLGPGPVLTVLALLLASTLA 628
                    LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL
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92JP-0301387.
92JP-0329546.
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39..286
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                                                                                                                                                                    Score 3053; DB 15;
Pred. No. 2.4e-270;
3; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                        has potential platelet function.
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Diagnosing carcinomas, e.g. adenocarcinoma or ovarian carcinomas, detecting reactivity of a molecule (with an antigenic determinant present in a sample) with an antibody specific for a mesothelin reantigen polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesothelin; mesothelin related antigen; MRA; malignant condition; cancer; differentiation antigen; adenocarcinoma; mesothelioma; ovarian carcinoma; pancreatic carcinoma; non-small cell lung carcinoma; MRA-2.
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                                                                                                                                                                                                                                                                                  Scholler NB,
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25-FEB-2000; 2000WO-US04834.
                                                                                                                                                                                                                                                       differentiation antigen; adenocarcinoma; mesothelioma; ovarian
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                                                                                                                   WO200050900-A2
                                                                                                                                                                                                                                pancreatic carcinoma; non-small cell lung carcinoma; MRA-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB08543 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 48; Fig 7A-B; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGIPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAP 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1547; DB 21;
Pred. No. 7.5e-133;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 402;
                                                                                                                                                                                                                                                             carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                     Megakaryoctye potentiator; Meg-Pot; thrombocytopenia; platelet; amplification; primer; polymerase chain rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human mesothelin related antigen (MRA)-1. Antibodies specific to MRA polypeptides are used for the detection of a malignant condition. Mesothelin is a differentiation antigen which is expressed in the surfaces of normal mesothelial cells and also on certain cancer cells, including epithelial ovarian tumours and mesotheliomas. The method is useful for detecting the presence of a malignant condition, specifically, adenocarcinoma, mesothelioma, ovarian carcinoma, pancreatic carcinoma or non-small cell lung carcinoma.
                                                                                 08-DEC-1994
                                                        Meg-Pot fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 48; Fig 5A-B; 92pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
05-AUG-1999;
                                                                                                                                                                                                     594 VLDLSVQ
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                                                                                                                                                                                                                                                                                                                                     114
                                                                                                                                                                                                                                                                                                                                                                                                                           293
                                                                                                                                                                                                                                                                                                                                                                                             354 LDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRP
                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                     CDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLR
                                                                                                                                                                                                                                                                                                                                                                                ldelypqgypesviqhlgylflkmspedirkwnvtsletlkallevnkghems-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ing carcinomas, e.g. adenocarcinoma or ovarian carcinomas, by
ng reactivity of a molecule (with an antigenic determinant and
in a sample) with an antibody specific for a mesothelin related
polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                               standard; peptide; 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                 600
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99US-0147404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.98;
97.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1531; DB 21;
Pred. No. 2.2e-131;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hellstrom
                       reaction;
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                       PCR.
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RESULT
AAR53988
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Best Local Similarity
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                      23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
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11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of the primers given in AAQ77809-10 in PCR resulted fragments given in AAQ63971.

DNA encoding Meg-Pot has potential use in treatment of
                                                                                                                 25-OCT-1993;
                                                                                                                                                               11-MAY-1994.
                                                                                                                                                                                                              WO9410312-A
                                                                                                                                                                                                                                                                              Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    platelet.
                                                                                                                                                                                                                                                                                                                                                                                                                        Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meg-Pot N-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR53988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR53988 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \ensuremath{\mathsf{UNA}} encoding \ensuremath{\mathsf{Meg-Pot}} has potential use in treatment of thrombocytopenia and low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 51; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mega:karyoctye potentiator -
thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-167467/20.
N-PSDB; AAQ63971.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9410312-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 LNPDA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%; Score 325; DB 15; llarity 100.0%; Pred. No. 2.8e-22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                   92JP-0286153.
92JP-0301387.
92JP-0329546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92JP-0301387
92JP-0329546
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                                                                                                                   93WO-JP01540
                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                           /note= "residue not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oh-eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Yamaguchi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT
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Best Local Similarity 97.1%;
Matches 34; Conservative
                                                                                                                                                                                                                  23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR53990;
Sequence
                    Use of the primers given in AAQ77805-08 in fragments given in AAQ63969-70.
DNA encoding Meg-Pot has potential use in the thrombocytopenia and low platelet function.
                                                                                                  New mega: karyoctye\ potentiator\ \cdot\ for\ potential\ treatment\ thrombocytopenia
                                                                                                                                    WPI; 1994-167467/20
N-PSDB; AAQ63970.
                                                                                                                                                                                                                                                                                                                                                        Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
platelet; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                                                                                                                          Meg-Pot fragment
                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR53990 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Meg-Pot thrombocytopenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-167467/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori K,
                                                                             Disclosure; Page 50; 74pp; Japanese
                                                                                                                                                                       Hattori K,
                                                                                                                                                                                                                                                                25-OCT-1993;
                                                                                                                                                                                                                                                                                      11-MAY-1994
                                                                                                                                                                                                                                                                                                            W09410312-A
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mega:karyoctye potentiator -
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                                                                                                                                                                                           (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 AA;
25 AA;
                                                                                                                                                                      Kojima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kojima T,
                                                                                                                                                                                                                  92JP-0286153.
92JP-0301387.
92JP-0329546.
                                                                                                                                                                                                                                                                93WO-JP01540
                   has potential use in treatment low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               has potential use in treatment low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74pp; Japanese
                                                                                                                                                                       Oh-eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oh-eda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163; DB 15;
Pred. No. 7.1e-08;
0; Mismatches 1
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                                                                                                                                                                       Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potential
                                                        PCR resulted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Query Match Best Local Similarity

3.9%;

Score 128; DB 15; Pred. No. 6.7e-05;

Length 25;

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RESULT
AAE03600
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                                                                                                                                                                                                                                                                                                                                                                                                                                           amyotrophic lateral sclerosis; epilepsy; psychiatric disorder; mania; depression; schizophrenia; anxiety; phobic disorder; learning disorder; memory disorder; amnesia; migraine; protein protein interaction; cellular activity; neoplastic transformation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leucine-rich repeat-containing protein, AZAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE03600 standard; Protein;
                                             Region
                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostate cancer; genitourinary system carcinoma; testicular tumour;
Alzheimer's disease; dementia; Parkinson's disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS disorder; central nervous system disorder; prostate di prostatitis; benign prostatic hyperplasia; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; leucine-rich repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    identification; gene therapy.
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59..794
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                 /note= "Leucine-rich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                         leucine-rich repeat (LRR)"
               repeat (LRR)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate disorder;
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FFFF
                                                                                                                                                                                                                                                            disorders e.g. amnesia or age-related memory loss, and neurological disorders e.g. migraine. AZAD molecules are useful as markers of disorders or disease states, as markers for precursors of disease state, for predisposition of disease state or as markers of drug activity or pharmacogenomic profile of a subject. The AZAD polypeptide and polynucleotide are capable of modulating protein-protein interaction, e.g. by interacting with an extracellular component, thereby modulating cellular activities, including attachment, adhesion, migration, patterning, growth and/or differentiation of a cell. AZAD proteins regulate embryonic development and differentiation, tissue maintenance and function, pathological conditions, e.g. neuronal degeneration, neoplastic transformation and tumour progression. AZAD proteins are
                                                                                                                                                               useful as immunogens to raise anti-AzAD antibodies which are useful to detect and isolate AZAD proteins and modulate its activity. AZAD proteins are useful to screen for naturally occurring AZAD substrates and to screen for drugs or compounds which modulate AZAD activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and cancer (e.g. adenocarcinoma, prostate cancer, genitourinary system carcinomas and testicular tumour). The neurodegenerative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosing AZAD-mediated or related disorders, which includes a neural disorder (e.g. neurodegenerative disorders, including CNS disorders)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human leucine-rich repeat-containing secreted protein, AZAD AZAD polypeptide is useful for identifying a compound which modulates its activity and binds to it. AZAD proteins and nucleic acid molecules are useful for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New leucine-rich repeat-containing protein and nucleic acid molecules for diagnosing, treating neural disorders, such as neurodegenerative disorders, such as Alzheimer's disease, dementia, epilepsy and prostate
                                           the AZAD protein are useful in gene therapy. AZAD sequences are also useful to map their respective genes on a chromosome, for tissue type and in forensic identification of a biological sample.
                                                                                                                   AZAD nucleic acid fragments are useful as primers or hybridisation probes for the detection of AZAD-encoding nucleic acids. cDNA encoding nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy, psychiatric disorders e.g. depression, schizophrenic disorders, mania, anxiety or phobic disorders, learning or memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and a prostate disorder, e.g. prostatitis, benign prostatic hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-381633/40.
N-PSDB; AAD08044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Khodadoust
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676..6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mour). The neurodegenerative disorders
dementias related to Alzheimer's disease.
                                                                                                                   nucleic acids. cDNA encoding
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Query Match Best Local Similarity

3.8%;

Score Pred.

123.5; DB No. 0.037;

22;

Length 794;

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Sequence

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                                                                                                          The present invention relates to human JAFFA polyhuclevilves (New AAF90326) and polyheptides (see AAB82351). JAFFA is a novel membe of the fibroblast growth factor family. JAFFA proteins may be useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as cancers and ABO(H) blood group disorders, and for controlling cellular proliferative and/or disorders, and for controlling cellular proliferative and/or
                        differentiative disorders. JÄFFA nucleic acids and proteins may be used to treat and/or diagnose a variety of immune disorders such as autoimmune disease and multiple sclerosis. JAFFA nucleic acids may also be used to express JAFFA protein, to detect JAFFA mRNA or a genetic alteration in a JAFFA gene, and to modulate JAFFA activity. Note: The present sequence is given in the Sequence Listing from
                                                                                                                                                                                                                                                                          Isolated JAFFA nucleic acid molecules which encode novel fibroblast growth factor family members (JAFFA) are useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB82352 standard; Protein;
                                                                                                                                                                                                                             Disclosure; Page 129-131; 137pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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            the present invention, but does not
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within the specification
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                   Nakagawa
Tateishi
                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                          Coryneform bacterium; ar organic acid synthesis.
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                                                 Claim 17;
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nes 72; Conserv
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DB; AAH66664.
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; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda
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Ozaki A;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. are useful for identifying the mutation point of a gene derived from

of coryneform bacterium,

measuring expression

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Matches 136
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                           AAG38205;
                                                  AAG38205 standard; Protein; 349
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05-MAY-1999;
06-MAY-1999;
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Arabidopsis thaliana protein fragment SEQ ID NO: 47099

Protein identification; signal transduction hybridisation assay; genetic mapping; gene ε on; signal transduction pathway; metabolic genetic mapping; gene expression control; pathway;
promoter;

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06-JUL-1999; 08-JUL-1999; 09-JUL-1999; 12-JUL-1999; 13-JUL-1999;

14-JUL-1999; 15-JUL-1999; 16-JUL-1999; 16-JUL-1999; 23-JUN-1999; 24-JUN-1999; 28-JUN-1999; 29-JUN-1999; 30-JUN-1999; 01-JUL-1999; 01-JUL-1999; 02-JUL-1999;

21-JUN-1999; 22-JUN-1999; 23-JUN-1999;

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                                  easastirrahavhpitavqiewslwsrdaeediipicrelgigivaysplgrgflaagp
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l Similarity 20.7%;
92; Conservative (
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9908-015263

9908-0153758

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53; Mismatches
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                                                                                                                  WPI; 1994-167467/20.
N-PSDB; AAQ63969.
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Use of the primers given in AAQ77805-08 in
                               Disclosure; Page 50; 74pp; Japanese
                                                                                                                                                                 Hattori K, Kojima T,
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                                                               thrombocytopenia
                                                                               New mega:karyoctye potentiator
                                                                                                                                                                                                  (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 DIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLT
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92JP-0329546.
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                                                                                                                                                                                 This invention describes a novel human phospholipase A2 (PLA2) protein (I) and its encoding nucleic acid. The amino acid (I) releases arachidonic acid in specific tissues characterized by unique membrane phospholipids, by generating lysophospholipid species which are deleterious to membrane integrity or by remodeling of unsaturated species of membrane phospholipids through deacylation/reacylation mechanisms. The amino acid is useful in assays to identify inhibitors having a therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of Alzheimer's disease. The amino acid (I) allows sensitive and rapid screening and identification of inhibitors of phospholipase A2. This sequence represents the human PLA2 protein (also known as phosphatide 2-acyl hydrolase).
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                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Column 53-58; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated amino acid having phospholipase (PL)A2 activity is useful in assays to identify inhibitors having a therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PLA2 protein.
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DNA encoding Meg-Pot has potent
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phlclldvgyli-----ntscl
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Search completed: December 7, 2001, 10:01:37 Job time: 720 sec

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US-08-426-819A-18
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US-08-689-276A-3
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PCT-US95-15327-2
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ALIGNMENTS

RESULT 1 US-08-776-271-2

Sequence 2, Application Patent No. 6083502 GENERAL INFORMATION:

Application

US/08776271

APPLICANT: Pastan, Ira
APPLICANT: Chang, Kai
TITLE OF INVENTION: MeTITLE OF INVENTION: Pri
TITLE OF INVENTION: an

Mesothelin, a Differentiation Antigen Present on Mesothelium, Mesotheliomas and Ovarian Cancers and Methods and Kits for Targeting the Antigen

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US-08-776-271-2
                                                                                                                                                                       CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/00224
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,166
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUBBER: 41,739
REFIRENCE/DOCKET NUMBER: 015280-259100US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/776,271
FILING DATE: 01-DEC-1998
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CITY: San Francisco
STATE: California
COUNTRY: USA
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- NO: 2:
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Query Match

100.0%;

Score 3261;

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Length 628;

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RESULT 2
US-09-215-035-2
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Patent No
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                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IFOOPPY
COMPUTER: COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             APPLICANT: Pastan, Ira
APPLICANT: Chang, Kai
TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
CITY: San Francisco
STATE: California
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                           APPLICATION
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No. 6153430
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                                                      PatentIn Release #1.0,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/010,166
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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FILING DATE: 03-JAN-
PRIOR APPLICATION DATA:
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LENGTH: 628 amino acids
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APPLICATION NUMBER:
FILING DATE: 01-DEC-
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                                                                TVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGIPNGYLVLDLSVQ
                                                                                                                                       VLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTDAVLPL
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                                     ETLSGTPCLLGPGPVLTVLALLLASTLA
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                                                                                                                                                                                   IDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLD
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03-JAN-1997
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Pred. No. 1.5e-303;
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Best Local Similarity
Matches 601; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ
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APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Genes Coding for Megakaryocyte TITLE OF INVENTION: Potentiator NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/426,819A
FILING DATE: 21-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Birch, St
STREET: P.O. Box 747
CITY: Falls Church
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                                                  SVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKT 298
                                                                                                                                      DVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTW 238
                                                                                                                                                                                                         DLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEA 178
                                                                                                                      DVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTW
                                                                                                                                                                                                                                                                           LSPRQLIGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL 118
                                                                                                                                                                                                                                                                                                                            MALPTARPLLGSCGTPALGSLLFLLFSLGWVQPSRTLAGETGQEAAPLDGVLANPPNISS
                    ACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELY
                                                                                                                                                                                         DLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEA 180
                                                                                                                                                                                                                                                          LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL 120
22040-0747
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Oh-Eda, Masayoshi
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95.48;
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Pred. No. 7.8e-284;
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                                                                                                                                     TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                 NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28.977
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,819A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 747
CITY: Falls Church
STATE: Virainia
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NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yamayuu...APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Oh-Eda, Masayoshi
HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFÓRMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                       MOLECULE TYPE:
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                                                            TOPOLOGY: not
                                                                                               TYPE: amino acid
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                                                                                                                  LENGTH:
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                                                                                                                    584 amino acids
                                                        NSS: not relevant not relevant
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Query Match
Best Local Similarity
Matches 576; Conserv

Conservative

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Score 2956; DB 1; Pred. No. 2.1e-274; 2; Mismatches 6;

Length 584; Indels

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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,819A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
A,
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ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                        ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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APPLICANT: Hattori, Kunihiro
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22040-0747
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Oh-Eda, Masayoshi
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                          , Gerald M.
ER: 28,977
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                                                                                                                                       Version
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08426819A Patent No. 5723318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.6
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-205-000 37:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
                                                                                                                                                                                                                                                                                                      APPLICANT: Yamaguchi, No. 5723
APPLICANT: Kojima, Tetsuo
APPLICANT: Kojima, Tetsuo
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Codi
TITLE OF INVENTION: Potentiato
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                           ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: no MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
            ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 21-APR-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 PSWRQPER 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                             ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-205-8050
                                                                                                                                                                                             COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSWRQPER 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RORLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD
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                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703-205-8000
                                                                       21-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
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                                                                                                                                                                                                                                                                                                         Potentiator 37
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                                                                                         US/08/426,819A
              28,977
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230-107P
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                                                                                                                                                                                                                                                                                                                                      for Megakaryocyte
                                                                                                                        Version
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2.5e-111;
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TELECOMMUNICATION INFORMATION:

ELEPHONE:

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US-08-426-819A-19
; Sequence 19, Application US/08426819A
; Patent No. 5723318
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Best Local Similarity 100
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/426
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M.
NAME: MUTPHY JT., Gerald M.
REGISTRATION UNBER: 28,977
REFERENCE/DOCKET NUMBER: 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-20 NFORMATION FOR SEQ
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MEDIUM TYPE: Floppy disk
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                                                                                                                                              MOLECULE TYPE: PHYPOTHETICAL: NO FRAGMENT TYPE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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                                                                                                       MMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LNPDA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
NAME/KEY:
                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                  40 amino acids
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Oh-Eda, Masayoshi
                                                                                                                                                                                                                                                          not relevant
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 572331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.4%; Score 210; DB 1; Best Local Similarity 100.0%; Pred. No. 2.5e-13;
                               TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 747
CITY: Falls Church
STATE: Virain:
                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,81: FILING DATE: 21-APR-1995
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 DALRGLLPVLGQPIIRSIPQGTVAAWRQRSSRDPSWRQPE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..16
OTHER INFORMATION: /label= fragment
OTHER INFORMATION: /note= "sequence of cyanogen bromide fragment representing
OTHER INFORMATION: C-terminus of MegPOT determined in Example 28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                             NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
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OTHER INFORMATION:
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                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                              TELEPHONE:
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Oh-Eda, Masayoshi
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35
                                                  703-205-8050
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                                                                                                                                                                         21-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                          Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Coding
                                                                                                                                                                                                                                                                                                                                                                                                                                             Potentiator
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                                                                                                                                                                                                                               Version #1.30
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APPLICANT: Gustafsson, Claes
APPLICANT: Betlach, Mary C.
APPLICANT: Betlach, Mary C.
APPLICANT: Ashley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Ziermann, Rainer
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 30062-20020.20
CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT APPLICATION NUMBER: 09/010,809
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
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; ORGANISM: Sorangium cellulosum
US-09-144-085-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Pate
SEQ ID NO 2
LENGTH: 6095
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 143; Conserva
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Best Local Similarity
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                                                     3083 QLEQELAAKVKGAWHLHQLLGKRELDAFVLYGSIAGLWGSGAQA----GYGAANAGLDAL 3138
                                                                                                                                3030 RGIRVTLAACDVS----ERA-QLAALLAE--LEQDEAPLRAVAHLAGIGRRVPLRELEPE 3082
                                                                                                                                                                                                           2975 GWKPRGTVLITGGVGGLGGHLARWLAGR-GAEHL----VLASRRGASAPGASELRDELVA 3029
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HYPOTHETICAL: NO
FRAGMENT TYPE: 11
                                                                                              112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide LOCATION: 1..35 OTHER INFORMATION: OTHER INFORMATION:
                   151 PRGAPERQRLLPAALACWG-
                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: not
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                                                                                            DLD-----ALPLDLLLFLNP-DAF-----
                                                                                                                                                                     ----LGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAH------RLSE-PPE 111
                                                                                                                                                                                                                                                GDRPGSLLFLLFSLGWV--HPARTLAGETGTESAPLGGVLTTPHNISSLSPRQL-----
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                                                                                                                                                                                                                                                                                                        4.1%; Score 134; DB 4; Length 6095; 23.6%; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.0%; Score 163; DB 1; 97.1%; Pred. No. 6.4e-09
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/note= "region of Glu-C peptide having low
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/note- "
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                 --VRGSLLSEADVRALGGLACDLP-G 192
                                                                                            --SGPQACTRFFSRITKANVDLL 150
                                                                                                                                                                                                                                                                                      217;
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                                                                                                                        TELEFAX: (617)
INFORMATION FOR SEQ
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
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  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                       TOPOLOGY:
                                      STRANDEDNESS
                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
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                                                           amino acid
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87 CambridgePark Drive
                                                                                778 amino acids
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                     linear
                                                                                                                                                                 (617) 498-8224
protein
                                                                                                                  7) %5.
) 876-5851
NO: 2:
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RESULT 11
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                                                                                                                                                                       Sequence 4, Application US/09460145
Patent No. 6287838
GENERAL INFORMATION:
APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                       STREET: 87 Cambridge CITY: Cambridge STATE: MA
                                                                                                                                                    CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
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                         COUNTRY: U
ZIP: 02140
                                                                                                          ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 QSLADR---
  539 --PLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLQLQGGIPN-----
                                                                                                                                                                              439 LTAFYPGYLCSLSPEELSSVPPSSIWAVRFQDLDTCD--PRQLDVLYPKARLAF-QNMNG
                                                                                                                                                                                                                          416 --NLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCAL----NTKGQ-----S
                                                                                                                                                                                                                                                                 384 KWNVTSLETLKALLEVDKGHEMSPQAP-----RRPLPQVATLIDRFVKGRGQLDKDTLDT 438
                                                                                                                                                                                                                                                                                                                                                                                                           351 SGSTWALANLYEDPEWSQKD------LAGPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LDGDLQEDEIPVVAIMATGGG------IRAMTSLYGQLAGLKELGLLDCVSYITGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 CPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQ-----PIIRSIPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QVVRLVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 HRVQLVV--PGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLSALPSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 MELKVFDQDLVTGDDP--VLSVLFDAGTLR-----AGEFRRESFSLSPQGEGRLEVEFRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                     SEYFVKIQSFL--GGAPTE--DLKALSQQNVSMDLATFMKLR--
                                                                                                                                                                                                                                                                                                                                                          CVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIR 383
                                            NLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVAAWRQRS-SRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEA 323
                                                                                                                                  LTTFEEGEWCEFSPYEVGF---PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWS
                                                                                                                                                                                                                                                                                                                  ----ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFT----
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OY 117 PLDLLLELNPDAFSGPQACTRFF-SRITKANVDLLPRGAPERQRLLPAALACWG 169 . : : : : : : : : :	Oy 57 SSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDAL 116	OY 1 MALQRLDPCWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTESAPLG-GVLTTPHNI 56	Query Match 3.5%; Score 113.5; DB 3; Length 913; Best Local Similarity 20.8%; Pred. No. 0.076; Matches 143; Conservative 72; Mismatches 257; Indels 215; Gaps 33;		; SEQUENCE CHARACTERISTICS: ; LENGTH: 913 amino acids ; TYPE: amino acid	: TELEPHONE: (317) 276-0756 ; TELEPAX: (317) 276-3861 : TELEPAX: (317) 276-3861	; NAME: Gaylo, Paul J. ; REGISTATION NUMBER: 36,808 ; REFERENCE/DOCKET NUMBER: X-10610 . TEFECOMMINICATION TOPOMOTION.	; APPLICATION UMBER: US 60/041,264 ; FILING DATE: 19-MAR-1997 ; ATTORNEY/AGENT INFORMATION:	; APPLICATION NUMBER: US 60/014,608 ; APPLICATION NUMBER: US 60/014,608 ; ETILING DATE: 29-MAR-1996 ; ETILING DATE: 29-MAR-1996	APPLICATION NUMBER: US/08/827,208 FILING DATE: 28-MAR-1997 CLASSIFICATION: 435	AT ST	ZIP: 46285 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk		OF INVENTION: NUCLEIC ACID COMPOUNDS ROF SEQUENCES: 4 RESSEE: Elitible and Company	; APPLICANT: SHRIP, JOHN D. ; APPLICANT: Strifler, Beth A. ; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED	Kramer, Ruth M. Pickard, Richard	; Sequence 3, Application US/08827208 ; Patent NO. 6025178 ; GENERAL INFORMATION:	RESULT 12 US 08-827-208-3	QY 591	579 WRPLAQATHNFLRGLHFHKDYFQHPH	= -
; APPLICATION NUMBER: US 60/014,608 ; APPLICATION NUMBER: US 60/014,608 ; FILING DATE: 29-MAR-1996	2 4 0	; OPERALING SISTEM: PC-DOSMS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/500,358	COUNTRY: United States of America ; ZIP: 46285 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; COMPUTER: TEM PC compatible	RET: Lilly Corporate Ce	; ITITLE OF INVENTION: NUCLEIC ACID COMPOUNDS ; NUMBER OF SEQUENCES: 4 ; CORRESPONDENCE ADDRESS: ADDRESSE: Eli Lilly and Company	CANT:	; APPLICANT: Chiou, Xue-Chiou C. ; APPLICANT: Kramer, Ruth M. ; APPLICANT: Pickard, Richard T.	Sequence 3, Application US/09500358; Patent No. 6197569; GENERAL INFORMATION:		Oy 591GYLVLDLSVQETLSCTPCL 609 : Db 741 PHLCLLDVGYLINTSCL 757	Qy 539PLTVAEVQKLLGPHYEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGI	635 ×	578	532	OV 384 KWNVTSLETLKALLEVDKGHEMSPOAPRRPLPOVATLIDRFVKGRGO	324 CV	Qy 265 IVAAWRQRS-SRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIF	OY 209 CPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQP : : : : : : : : : : : :	_	170	Db 299 HRVQLVVPGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKA

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/STMDALRGLLPVLGQ----PIIRSIPQG 264
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IRAMTSLYGQLAGLKELGLLDCVSYITGA 466
                                                                                                                                                                                                                                                                                                                   ----KATTLD-----GLPNQLTPSE 740
               ILRQRQDDLDTLGLGLQGGIPN----- 590
                                            KEQVPLLKIEEPPSTAGRIAEFFTDLLT 694
                                                                  MDLATEMKLR------TDAVL 538
                                                                                     LDTCD--PRQLDVLYPKARLAF-QNMNG 495
                                                                                                                                  --LAGPT----- 491
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PRIOR APPLICATION DATA: APPLICATION NUMBER:

US 60/041,264

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (317) 276-0756
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                                                                              695 WRPLAQATHNFLRGLHFH--KDYFQHPHFSTW----KATTLD------GLPNQLTPSE 740
                                                                                                                                                          635 NLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLT 694
                                                                                                                                                                                                                                                                                                                                                                                                                                     324 CVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIR 383
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    741
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                                                                                                                                                                                                                                                                                                                                                     384 KWNVTSLETLKALLEVDKGHEMSPQAP-----RRPLPQVATLIDRFVKGRGQLDKDTLDT 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MALQRLDPCWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTES---APLG-GVLTTPHNI 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVAAWRORS-SRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQ-----PIIRSIPQG
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                                                                                                                                                                                                                                                                           LTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCD--PRQLDVLYPKARLAF-QNMNG
    PHECLEDVGYLI -----
                                       -----GYLVLDLSVQETLSGTPCL 609
                                                                                                                                                                                               SEYFVKIQSFL--GGAPTE--DLKALSQQNVSMDLATFMKLR----
                                                                                                                                                                                                                                      LTTFEFGEWCEFSPYEVGF----PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWS
                                                                                                                                                                                                                                                                                                                    --NLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCAL----NTKGQ-----
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-498-809-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gaylo, Paul J.
REGISTATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 913 amino acids
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NAME: Gaylo, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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417 LDGDLQEDEIPVVAIMATGGG-----IRAMTSLYGQLAGLKELGLLDCVSYITGA 460
                                         209 CPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQ----PIIRSIPQG
                                                                                    357 QVVRLVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQ 416
                                                                                                                                                                         299 HRVQLVV--PGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLSALPSG
                                                                                                                                                                                                                    117 PLDLLLFLNPDAFSGPQACT-----RFF-SRITKANVDLLPRGAPERQRLLPAALACWG
                                                                                                                                                                                                                                                                                                                                                  208 MELKVFDQDLVTGDDP--VLSVLFDAGTLR-----AGEFRRESFSLSPQGEGRLEVEFRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharp, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chiou, Xue-Chiou C.
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19-MAR-1997
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                                                                                                                                -VRGSLLSEADVR-'---ALGGLACDLPGRFVAESAEVL---LPRLVS
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US-08-426-819A-18
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GENERAL INFORMATION:
                                                                                                                                                         AFFLICATION NUMBER: 20-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mulphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                    TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/426,819A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Coding
TITLE OF INVENTION: Potentiator
NUMBER OF SEQUENCES: 37
                 TOPOLOGY: no
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                                                                                                                           TELEPHONE: 703-205-8050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                   STRANDEDNESS:
                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22040-0747
                                                                                       LENGTH:
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5723318
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Oh-Eda, Masayoshi
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LOCATION: 6.18
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Search completed: December Job time: 706 sec
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// Cgn2_6/ptodata/2/paa/US08_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

မ 8	765	4321	Result
559 482	1531 1247 579.5	3055 2956 1547	Score
17.1 14.8	46.9 38.2 17.8	93.7 90.6 47.4 47.4	Query Match
144 122	399 248 175	622 584 328 402	Query Match Length DB
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Sequence 599, App Sequence 702, App	Sequence 1, Appli Sequence 37, Appl Sequence 733, App	Sequence 35, Appl Sequence 36, Appl Sequence 2, Appli Sequence 13, Appl	Description

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e 10829	equence 13306,	e 2033,			3170	e 205	35,	Sequence 22, Appl	93,	e 93,	e 276:	e 35218,	Ø	e 8331,	e 1076,	e 794, A	O	13735,	e 519	10.	Sequence 2, Appli	e 2,	e 449,	e 970	51615,	e 532,	e 532,	8424,	Φ	100		19,	e 404	33, Ap	Sequence 406, App

ALIGNMENTS

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US-08-426-819-35
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           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/08/426,819
FILLING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUIPBY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Coc
TITLE OF INVENTION: Potentiat
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yamaguchi, Nozomi
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CITY: Falls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                               ZIP:
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22040-0747
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O. Box 747
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TELEPHONE:

703-205-8000

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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                  Sequence 36, Application US/08426819 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 93.7%;
Best Local Similarity 95.4%;
Matches 601; Conservative
                            APPLICANT: Yamaguchi, Nozomi
APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Edd, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Coding for INTERTION: Optentiator
NUMBER OF SEQUENCES: 37
                CORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELY 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVNKGHEMS-----PQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKT 298
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Birch,
                ADDRESS
 Stewart, Kolasch & Birch
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LENGTH: 584 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; POPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-426-819-36
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Best Local
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ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JI., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                            517
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CITY: Fa
STATE: V
COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 21-APR-1995
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les 576; Conserv
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               LSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDD
                                                                                                                                      LEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELS
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LSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDD
                                                                                                                      LEVNKGHEMS------PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELS
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Pred. No. 1.7e-266;
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276 180 216 120 156 60 96

336 240

472 516 412 456 360 396 300

532 576

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CURRENT APPLICATION NUMBER: US/09/513,597; CURRENT FILING DATE: 2000-02-25; NUMBER OF SEQ ID NOS: 18; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 2; SEQ ID NO 2; LENGTH: 328; TYPE: PRT; ORGANISM: Homo sapien
US-09-513-597-2
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US-09-513-597-2
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                               CURRENT APPLICATION NUMBER: US/09/513,597
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 13
LENGTH: 402
                                                                                                                                                                                                                                                               Sequence 13, Application US/09513597 GENERAL INFORMATION:
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Best Local Similarity
Matches 301; Conserva
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APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: CARCINOMAS
FILE REFERENCE: 730033.410
                                                                                                                                                APPLICANT: Scholler, Nathalie B. APPLICANT: Hellstrom, Ingegerd APPLICANT: Hellstrom, Karl Erik TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: CARCINOMAS FILE REFERENCE: 730033.410
ORGANISM: Homo sapien
                   TYPE: PRT
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                                                                         FastSEQ for Windows Version 4.0
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97.18;
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Pred. No. 3.6e-135;
1; Mismatches 0;
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APPLICANT: Scholler, Nathalie B.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: CARCINOMAS
FILE REFERENCE: 730033.410
CURRENT APPLICATION NUMBER: US/09/513,597
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 18
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-513-597-1
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LENGTH: 399
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Best Local
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                                                                                                                                                                                                                      Local Similarity
es 298; Conserv
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           CDPRQLDVLYPKARLAFQNMNGSEYFVKIOSFLGGAPTEDLKALSQQNVSMDLATFMKLR
                                                   CDPRQLDVLYPKARLAFQNMNGSEYFVKTQSFLGGAPTEDLKALSQQNVSMDLATFMKLR
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milarity 97.1%;
Conservative
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97.1%;
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Pred. No. 5.1e-135;
                                                                                                                                                                                                                                Score 1531; DB 19;
Pred. No. 1.6e-133;
                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                             Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
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CITY: Falls Church
STATE: Viraini
                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/426,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                    217
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                                                                                                                                                                                                                                             Local Similarity
mes 242; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                              GETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLST 96
                                                               RQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD 216
                                                                                                                             EQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPE 156
QQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRD 276
                                                RQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD
                                                                                                              EQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPE 120
                                                                                                                                                                              GETGQEAAPLDGVLANPPNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLST 60
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Pred. No. 2.6e-107;
Pred. No. 2.5e-107;
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SOFTWARE: FAST
SEQ ID NO 733
FRIGHH: 175
                                                                                                                                                                                                                   Sequence 599, Application US/09330360 GENERAL INFORMATION:
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APPLICANT:
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Best Local Similarity
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                         CURRENT APPLICATION NUMBER: US/09/330,360 CURRENT FILING DATE: 1999-06-11
                                                                                                                         APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/330,360 CURRENT FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human Fetal Lung Library
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NUMBER OF SEQ ID NOS:
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                                                                                                              FILE REFERENCE:
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TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (1)...(33)
NAME/KEY: VARIANT
LOCATION: (1)...(175)
COTHER INFORMATION: Xaa = Any Amino
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Robison, Keith
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                                                                                                            MLN98-34pA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(33)
; NAME/KEY: VARIANT
; LOCATION: (1)...(144)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-330-360-599
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Best Local Similarity 86.0%;
Matches 117; Conservative
                                                                                                                                                                     Best Local Similarity 84.3
Matches 102; Conservative
                                                                                                                                                                                   Query Match
Best Local :
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equence 702, Application US/09330360 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
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                                                    LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL 118
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                                                                                                                                                                                 14.8%;
84.3%;
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Pred. No. 2.2e-43;
2; Mismatches 15;
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Pred. No. 2.7e-36;
2; Mismatches 15;
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RESULT 11
US-08-426-819-33
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GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF T
                                                                 APPLICANT: Yamaguchi, Nozomi
APPLICANT: Kojima, Tetsuo
APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Coding for Invention: Potentiator
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: )
NAME/KEY: SITE
LOCATION: (127)
OTHER INFORMATION: )
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE LOCATION: (56) OTHER INFORMATION:
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LOCATION: (131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
LOCATION: (117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 134
                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, St
                                                                                                                                                                                                                                                                                                                                          383 RKWNVTSLETLKALLEVDKGHEMSPQ 408
                                                                                                                                                                                                                                                                                                                                                                                                 323 ACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 QGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELE 322
                                                                                                                                                                                                                                                                                                          100 RKWNVTSLETLKALLEVXKGHEMSPQ 125
                      STREET:
                                                                                                                                                                                                                                                                                                                                                                               40 TCVDAALLATQXDRVNXIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPXDI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 RGSGGKWR------RQPVLQQEGPRDRREPH------LLQEVGAG------------ 39
: P.O. Box 7
Falls Church
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                    Birch, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%;
63.7%;
                                     Stewart, Kolasch & Birch
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                                                                                                            ror.
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                                                                                                          Megakaryocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

Virginia RY: USA 22040-0747

COUNTRY:

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US-09-758-458-404
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; MOLECULE TYPE:
US-08-426-819-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 404, Application US/09758458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                          NAME/KEY: SITE
LOCATION: (128)
OTHER INFORMATION: Xaa e
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa e
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/758,458 CURRENT FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 520
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PMO41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO:
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                         NAME/KEY: SITE LOCATION: (140)
                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   LENGTH: 144
TYPE: PRT
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/426,819
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
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                                                                                                                                                                                                                                                                              ID NO 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 LNPDA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LNPDA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 325; DB 8; llarity 100.0%; Pred. No. 4.5e-22; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                   2000-01-31
                                                                                                                          Xaa equals any of the naturally occurring L-amino acids
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                                                            equals any of the naturally occurring L-amino acids
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RESULT 13
US-08-426-819-19
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21P: 22040-074,
2IP: 22040-074,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC DOS/MS-DOS
CO
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                  FEATURE:
                                                                                            NAME/KEY: Peptide LOCATION: .1..40 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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NAME/KEY: Modified-site
                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                     CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Falls Church
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QRLDPCW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
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WENTION: Genes Coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kojima, Tetsuo
Oh-Eda, Masayoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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O. Box 747
                                                                                                                                                                                                                                                                                                                                      internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerald M. IR: 28,977
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47.5%;
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                                                             /label= fragment /note= "sequence of cyanogen bromide fragment of MegPOT fr cDNA in Table 3" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/426,819
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Pred. No. 1.1e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for Megakaryocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #1.30
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OTHER INFORMATION:

/product= "is Xaa in COS"

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US-08-426-819-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08426819 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                             TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JI., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: FEATURE:
                               CLONE:
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Birch, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Birch, Stev
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                         MOLECULE TYPE: po
HYPOTHETICAL: NO
FRAGMENT TYPE: in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Genes Coding for Megakaryocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 DALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1.16
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                             CLONE: HPCY5
NAME/KEY:
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/426,819
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
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LOCATION:
                                                                                                                               TYPE: amino
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site LOCATION: 37
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                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22040-0747
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                                                                                                                                                             ENGTH:
                                                                                                                                               amino acid
                                                                                                                                                                35 amino acids
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Oh-Eda, Masayoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Peptide
1..35
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                                                                         internal
                                                                                                   peptide
                                                                                                                                    not relevant
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y 100.0%; Pr
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/note= "sequence of cyanogen bromide fragment representing
C-terminus of MegPOT determined in Example 28"
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Pred. No. 1.1e-11;
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Sequence 10981, Application PC/TUS0114827

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 21272-104
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 16102
SOFTWARE: CUStom
SEQ ID NO 10981
LENGTH: 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: DOMAIN

LOCATION: (747)...(768)

OTHER INFORMATION: BY EMATRIX, accession number PRO0500B, p-value-4.316e-09, raw
OTHER INFORMATION: Score of 7.74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             194 RPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVRWLRLSHNALSVLAPEALAGLPALR 253
                                                                             415 RAVAGPRAPPRGPPRGPGEERAVAPCPRACVCVPESRHSSCEGCGLQAVPRGF-----
                                                                                                                                                         363 RPLLEW-----LARARVRSDG--ACQGPRRLRGEALDALRPWDLRCPGDAAQEEEELEE 414
                                                                                                                                                                                                                                    306 DGGALQALGPRAFA---HCPRLHTLDLRGNQLDTLPPLQGPGQLRRLRLQGNPLWCGCQA 362
                                                                                                                                                                                                                                                                                                                254 RLSLHHNELQALPGPV-----LSQARGLARLELGHNPLTYAGEEDGLALPGLRELLL
                                                                                                                223 AALQG-----GGPPYGPPSTWSVSTMDALRGLLPVLGQPI-----IRSIPQGIVAAWRQR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 5.0%;
Local Similarity 97.1%;
                                                                                                                                                                                                                                                                                                                                        72 VSGLSTERVRELAVALAQKNVKLSTEQLRCLAH-RLSEPP-----EDLDALP--LDLLL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                    15 RPGSL--LFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHN-ISSLSPRQLLGFPCAE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALP 117
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OTHER INFORMATION:
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                                    SSRDPSWRQPERTILRPRERREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLAT 332
                                                                                                                                                                                         -----WGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAAR
                                                                                                                                                                                                                                                                       -----FLNPDAFSGPQACTRFFSRITKAN-VDLLP----RGAPERQRLLPAALAC---- 167
----PS--DTQLLDLRRNHFPSVPRAAFP------GLGHLVSLHLQHCGIAELEAG
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23.3%;
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/note= "region of Glu-C
codons."
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Pred. No. 0.0063;
0; Mismatches 267
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Pred. No. 2.3e-07;
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619 738	559 691	501 642	448 588	390 552	333 512
LAIL 622 : LELI 741	EERHRPVRDWILRQRQDDLDTLGLGLQGGIPNGYLVLDLSVQETLSGTPCLLGPGPVLTV 618	KIOSFLGGAPTEDLKALSQONVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKA 558 :: : : : ::: : :	CSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFV 500	390 LETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYL 447	333 QMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTS 389 : : :

Search completed: December 7, 2001, 09:52:20 Job time: 248 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

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Result
No.
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Maximum
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Maximum Match 1008
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
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     22552210
22552210
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25552210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB BB
    seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US00_NEW_COMB.pep:*
                                                                                                                                                                                                                                                                                                                       Query
Match
    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-215-035-2
3261
1 MALQRLDPCWSCGDRPGSLL.....LLGPGPVLTVLALLLASTLA 628
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    В
     US-09-828-792-733
US-09-828-792-792
US-09-828-792-702
US-60-325-795-2
US-60-325-795-2
US-09-815-242-11925
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US-09-722-708-55
US-09-722-708-55
US-09-722-708-55
US-09-976-544-49
US-09-981-353-188
US-09-815-242-5117
US-09-815-242-5111
US-09-815-242-12811
US-09-815-242-12819
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US-09-819-935-2
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244.470 Million cell updates/sec
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Sequence 733, App Sequence 799, App Sequence 702, Appli Sequence 5064, Appli Sequence 5064, Appli Sequence 55, Appli Sequence 55, Appli Sequence 44, Appli Sequence 44, Appli Sequence 6629, Appli Sequence 5111, Appli Sequence 51074, Appli Sequence 5408, Appli Sequence 6555, Appli Sequence 31, Appli
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DLLLF	DLLLF			Match ocal Simi	, 0	Fas 733 175 T	APPLICATION APPLIC	REFERENCI NT APPLIC	INV INV IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	792-73 733,		8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8				9
NPDAFSGP	LNPDAFSGPQACTRF	LSPRQLLGFPCAEVSGLS	MALQRLDP-CWSCGDRP-GSLLFLLFSLGWVHP	ilarity Conserva		tSEQ for W	APPLICATION NUMBER: FILING DATE: 1999-0 APPLICATION NUMBER: FILING DATE: 1998-0 OF SEQ ID NOS: 110	9	5 -	3 Application ATION:		2.77			.7 .7 .7	œ
QA	CTRF	SGLSTERV SGLSTERV	DRP-GSI TPALGSI	17.8% 68.6% ative	} 5) Xaa ■ Any	Windows ns	1999-06-1: 1999-06-1: 1098-60, 1998-06-2: 1998-102	-34Pa UMBER: 2001-0	David P. Keith E. Douglas Nucleic A	SD		775 5 775 5 775 5 775 5 775 5				519
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XPV8	NVDLLPRO	ALAQKNVI 	SLGWVHPAI : SLGWVQPSI	e 579. . No. ismato	o Acid	ion 3.0	58	,792	Molecule:	92	ALIGNMENTS	9-589-726- 9-589-727- 9-589-728- 9-589-731- 9-589-731-	5 6 6 6	5 2 5 5	9599	-8
SSPASRRE	FSRITKANVDLLPRGAPERQRLL	LAVALAÇKNVKLSTEQLRC	RTLAGETO RTLAGETO	5; DB 5 2.4e-42; hes 23					s Derived		ľS	26-326 27-326 28-326 31-326 32-326	221-326	23-326 24-326 30-326	38-146 38-162 43-17 42-5053	16-6004
MWTCSE	L	RCLAHRLS	STESAPLO : SQEAAPLO	5; Length ; ; Indels					ed from							
XPVSSPASRRPMWTCSEGGSRATAAAACG	PAALAC	TERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPI 	LLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNIS 	175; 31	•				ರು			Sequence Sequence Sequence Sequence	Sequen Sequen Sequen	Sequen Sequen Sequen	Sequenc Sequenc Sequenc Sequenc	equen ·
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US-09-828-792-599

Sequence 599,

Application US/09828792

GENERAL INFORMATION:

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: LOCATION: (1)...(33)
: NAME/KEY: VARIAUT
: LOCATION: (1)...(144)
: OTHER INFORMATION: Xaa = Any Amino Acid
US-09-828-792-599
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-828-792-702
                                                                               SEQ ID NO 702
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E
APPLICANT: Holtzman, Dougla:
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Best Local Similarity
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                                                                                                PRIOR APPLICATION NUMBER: US/09/330,360
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FastSEQ for Windows Version 3
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
                                                                                                                                                                                                                                                               APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
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PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
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CURRENT FILING DATE: 2001-04-09
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ORGANISM: Homo sapiens
                   ORGANISM: Homo sapiens
                                           TYPE: PRT
FEATURE:
                                                              ENGTH: 122
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Pred. No. 9.9e-41;
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; TITLE OF INVENTION: NOVEL SECRETED PROTEINS AND FILE REFERENCE: P-14990
; CURRENT APPLICATION NUMBER: US/60/325,795
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEO ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; ELENGTH: 762
; TYPE: PAT
; ORGANISM: Homo sapiens
US-60-325-795-2
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; LOCATION: (1)...(33)
US-09-828-792-702
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Best Local Similarity
Matches 102; Conserv
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APPLICANT: Wang, He
APPLICANT: Zhi, Yu
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468 ALAGLGRLIYLYLSDNQLAGLSAAALEGAPR--
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                         QMDRVNAIPFTY---EQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTS
                                                                         ----PS--DTQLLDLRRNHFPSVPRAAFP-
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                                                                                                                                                                                                                                                                                                                                       -----FLNPDAFSGPQACTRFFSRITKAN-VDLLP----RGAPERQRLLPAALAC----
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                                                                                                         SSRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLAT
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Pred. No. 2.8e-34;
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                                                                       -GLGHLVSLHLQHCGIAELEAG
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US-09-815-242-11089
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SEQ ID NO 11089
LENGTH: 1159
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Best Local Similarity 20.2%;
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes
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APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                 DLPGRFVAESAEVLLPRL-----VSCPGPLDQDQQEAA-RAALQGGGPPYGPPSTWSVST 242
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NGIDGELSMKIFDLVEKFAGYGFNKSHSAAYALVSYQTLWLKTHFPAEFMAAVMTSEMDN 793
                                                                                                                 MDALRGLLPVLGQPIIRSIPQGIVAAW-----RQRSSRDPSWRQPERTILRPRFRR
                                                                                                                                                           FRPGPLQSGMVDNFIDRKHGREEVSYP---DAEYQHASLKPILE---PTYG-----
                                                                                                                                                                                                                                           LLKRSETTAVFQLESRGMKDLIKRLQPD-----
                                                                                                                                                                                                                                                                                   --GPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEADVRALGGLAC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149;
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Trawick, John D.
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                                                                           ---IILYQEQVMQIAQ-VLAGYTLGGADLLRRAMGKKKPEEMAKQRLVFKEGAEK 733
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                                   -----VEKTACPSGKKAREIDESLIFYK----KWELEACVDAALLATQMDR 336
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; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5064
                                                    NUMBL.. SOFTWARE: Fasts SEQ ID NO 5064
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GENERAL INFORM
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CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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                                                                                                                             NUMBER OF SEQ ID NOS:
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                                           LENGTH: 2
TYPE: PRT
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                                                                                                         FastSEQ
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Yamamoto, Robert T.
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Query Match 3.1 Best Local Similarity 21.7 Matches 138; Conservative

3.1%; but 21.7%; Pre 70;

Score 101.5; D Pred. No. 5.6; 70; Mismatches

DB 5; ; 216;

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                                 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith
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APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPS 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRLVEQGADGLNQAAPDELVKNLLFY-----VAKAPSQSPRIRALKEQY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDA-----LPLDLLLFLN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQLVIKEARNGLEQAKDAITEFIASQWNHEHLARVPELLTQVRGGLAMIPLERAATLLET 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGGLL-----RKLRQTQQMALVGLLR-----NQDVATSLGYLARVYARLEGLCREAPLGP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11925, Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
Trawick, John D.
Carr, Grant J.
                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert T.
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 11925
LENGTH: 956
                                                                                                                                                               RESULT 8
US-09-722-487-55
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US-09-815-242-11925
                                                                                       Sequence 55, Application US/09722487
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LQRLDP------CWSCGD----RPG------SLLFLLFSLGWVHPA--
                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING DNA METABOLIC PROPERTY AMINOGLYCOSIDE DERIVATIVES
CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       PQI-----LETQLRALFRA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VREGLGEEVEALAEEALPDAVGEAEEDARPAPLRAGERLQAIAASPGIASGPAHVQVAQR 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAKGFAGEIRVRLADSEAAPVSAKSLSKLLALGARRGQ-TLEFSAEPAIAEDALPALLAA
                                                                                                                                                                                                                                                                           EDIRKWNVTSLET-LKALLEVDKGHEMSPQAPRRPL----PQVATL 420
                                                                                                                                                                                                                                                                                                                 APDLATQEAEYRRVLDALDGRPLVARTLDVGGDKPLPYWPIPHEENPYLGLRGIRLTLQR
                                                                                                                                                                                                                                                                                                                                                 AALLATQ-----MDRVNAIPFTYEOLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSP 379
                                                                                                                                                                                                                                                                                                                                                                                                                         SWR-QPERTILRPRFRREVEKTACPSGKKAREID-----ESLIFYKKWELEACVD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGIPALVGAGAAVLGLEPGTALLLDGEHGWLQV--APSTEQLQQAAAERDARQQRQARAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRVLARLCGVEAPREPEQPYILVMDEVGPSDVARLDAQRVAGILTARGGATSHSAIIARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDPELAEQVQLRLNRGESAEAAWSRVVEDSAAQQEALHDALLAERAADLR------DLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F-----EFQPRGESPAHERERLLRAKRAVDEEIVGLVERSTVKAIREIFVTHREML 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAHRLSEPPEDL------DALPLDL-----LLFLNPDAFSGP---QACTR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GF------PCAEVSGLSTERVRELAVALAQKNVKLSTEQ------LRC 101
                                                                                                                                                                                                                                                                                                                                                                                       AQRLEPART -- RDGHAVEVCANLGDTAGAARAVELGAEGVGLLRTEFVFMNN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GPPSTWSVST------MDALRGLLPVLGQPIIRSIPQGIVA--AWRQRSSRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERLCDLLLEGRGAELVRATSSRSVLAALGGELPPDWPSARAVLANPHGLHA-RPAQALAQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%;
ilarity 22.0%;
Conservative 4
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Pred. No. 1.
                                                                                                                                                                                                                                         -AGERPLRVMFPMVGSL
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                                                       PROCESSES
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TOPOLOGY: linear;

MOLECULE TYPE: peptide;
SEQUENCE DESCRIPTION: S
US-09-722-487-55
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Best Local Similarity 20.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              149
                         377
                                                                                                                                                                                       277
                                                                                                                                              269
                                                                                                                                                                                                                               209
                                                                                                                                                                                                                                                                     240 VSTMDALRGLLP-----
                                                                                                                                                                                                                                                                                                                                                      192
                                                                                                                                                                                                                                                                                                                                                                                           115 RPPNQVTVAGISLPLANSPPGVPSQQ------LWG
                                                                                                                                                                                                                                                                                                                                                                                                                                   139 F--SRITKANVDL----LPRGAPERQRLLPAALACWGVRGSLLSEADVRALGGLACDL-P 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,487
FILING DATE: 28-Nov:2000
CLASSIFICATION - CURROWN>
PRIOR APPLICATION NUMBER: 09/179,58
APPLICATION NUMBER: 09/179,58
FILING DATE: CURROWN>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 DALPLDL----LLF------LNPDAF----LNPDAF-----SGPQACTRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 SLSPRQLLGFPCAEVSGLSTERVRELAV----ALAQKNVKLSTEQLRCLAHRLSEPPEDL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 PRDPSKSGSHGIFFKQQNPSSSSHGDQRPQNPHSFPPNTSEQAKGMWQRPEEMPTACPSY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SISP---LKCPCL----LQRSRGKKIEANRQKALARRAEKLLAEQHQKPAQSKQGPSQNL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
                                                                                                                                                                                  P---SW------RQPERTILRPRERRE--VEKTACPSGKKAREIDESLIFY 316
MSPEDIRKWNVTS-----LETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQ 430
                                                                                                                                                                                                                           GSVMPRTEGRLOOKAGTPMHRVVGSQQGRCIRNGERFQVKIGYNEALIAVFKSLPSRSYD
                                                                                                                                                                                                                                                                                                            GHPQASLETQSTPFANTTHEPLRKVKNFQETAASSSGQPPRDPELEARIGRPSTSGQNIS
                                                                                                                                                                                                                                                                                                                                                GRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGP-----PST----WS
                                                           AKTGLPAAPSLAFVKGQCVLISRARF---EADI------SYSEDLIA----LFKQ 358
                                                                                                 KKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLK 376
                                                                                                                                            PATKTWNFSMTDYGPLMKAAQRLPGIT-LQPLEGAEGHMESPSTSSG------II 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                   --VLGOPIIRSIPOG-----IVAAWRQRSSR--D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99.5;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 941;
                                                                                                                                                                                                                                                                                                                                                                                           ----CELGQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                           268
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RESULT 9
US-09-722-708-55
Sequence 55, Application US/09722708
GENERAL INFORMATION:
; molecule Type: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-722-708-55
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                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/722,708
FILING DATE: 28-NOV-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION UMBER: 09/179,558
FILING DATE: CUNKNOWN>
FILING DATE: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 --FLKNIKTAVCAAMP-----LLKVAKRVILLSGTPAMSRPAELYTQILAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503 NPLDINV-VVTGKDRLTDGLVNIVSFDLLSKLEKQLKPPFKVVIIDESH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               443 NFAIAQRGRLLLADDMGLGKTIQAICIAAYYRKEWPLLVVVPSSVRFTWEQAFCRWLPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 -----KARLAFQNMNG------SEYFVKIQSFLGGAPTED------LKAL 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 LDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 QDDLDTLGLGLQGGIPNGYLVLDLSVQE-TLSGTPCLLGPGPVLT-VLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 M---DSRKYDVKTRKWSFLLEEYSKLMERVRG---PPQVQLDPLPKTLTLF-----RAQ 406
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909990
TELEFAX: (212)78699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muthuswami, Robini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hockensmith, Joel W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQQNVSMDLATFMKLRTDAVLPLT----VAEVQKLLGPHVEGLKAEERHRPVRDWILRQR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 A. CITY: New York
                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: U.S. FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NY
                                                                                      STRANDEDNESS: single
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                                                                                                                                      LENGTH: 941 amino acids
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Query Match
Best Local Similarity

3.1%;

Score 99.5; Pred. No. 2; Mismatches

DB 5; 216;

Length 941; Indels 263;

Gaps

40;

Matches

148;

Conservative

83;

```
TYPE: PRT ORGANISM: Streptomyces venezuelae US-09-657-440-2
                                                                                                   APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE PO.
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
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                                                             SEQ ID NO 2
LENGTH: 3739
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09657440 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C..
APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPLDINV-VVTGKDRLTDGLVNIVSFDLLSKLEKQLKPPFKVVIIDESH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSPEDIRKWNVTS-----LETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQ 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKTGLPAAPSLAFVKGQCVLISRARF---EADI-----SYSEDLIA----LFKQ 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRDPSKSGSHGIFFKQQNPSSSSHGDQRPQNPHSFPPNTSEQAKGMWQRPEEMPTACPSY 114
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RESULT 11

US-60-325-795-4

Sequence 4, Application US/60325795

Sequence 4, Application:
GENERAL INFORMATION:
APPLICANT: Su, Eric W
APPLICANT: Shi, Yu
APPLICANT: Ehi, Yu
FITLE OF INVENTION: NOVEL SECRETED PROTEINS AND THEIR USES
FILE REFERENCE: P-14990
CURRENT APPLICATION NUMBER: US/60/325,795
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 10
SOCTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 610
Type: Der
                        Q
                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Homo sapiens US-60-325-795-4
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                                                         Query Match
Best Local Similarity
Matches 97; Conserv
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116 LPLDLLLELNP----DAFSGPQACTRFFSRITKA----NVDLLPRGAPE-RQRLLPÀALA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 DALPLDLLLELNPDAFSGPQACTRFFSRITKANVDLLPR-----GAPERQRLLPAALA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 DLSVQETLSGTPCLLGPGPVLTVLALLLASTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEVQKL-----LGPHVEGLKAEERHRPVRDWILRQRQDDLD-TLGLGLQGGIPNGYLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCRAG-GFLDEAG-EFDA---DFFGISPREALAMDPQQRLLLE--TSWEAVEDAGIDPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPVAIVGMACRLPGGVASPEDLWRLVAGGEDAISGFPQDRGWDV--EGLYDPDPDASGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NATGL-ALPATLVFD------YPTPRTLAEFLLAEILGEQAGAGEQLPVDGGVDD 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVTSLETLKALLEVDKGHEMSPQAPRRPLPQ-----VATLIDRFVKGRGQLDKD-TLDT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRELGALTGAEQQRRMQELVREHLAVVLNHPSPEAVDTGRAFRDLGFDSLTAVELRNRLK 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESV----IQHLGYLFLKMSPEDIRKW 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAHPLSAVLHLPPTVDSEPLAAT-------DADALARVVTAKATAALHLDRLLREAAA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTAFYPGYLCSL-----SPEEL------SSVPPSSIWAVRPQDLDTCDPRQLDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIADVDWSSFAPGFTTARP------GTLLADLPEARRALDEQQSTTAADDTVL 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQHRADGPTVTSVAWSPWEGSRVTEGATGERLRRLGLRPLAPATALTALDTALGHGDTAV 1384
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                                                                     Conservative 47;
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                                                                                           3.0%; Score 99; DB 6; Length 610; 24.9%; Pred. No. 1.2;
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                                                                   Mismatches 152; Indels 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 234;
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US-09-976-594-449
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GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PERL Program
SEQ ID NO 449
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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                                                                                                                                 100
                                                                                                                                                                      137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 GHNPLTYAGEEDGLALPGLRELLLDGGALQALGPRAFAHCPRLHTLDLRGNQLDTLPPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 DESLIFYKKWE-----LEACVDAALLATOMDRVNAIPFTYEQLDVLKHKLDELYP-Q
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                 228 GGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTIL 287
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                                                                                                                                                                                                                                                                                                                      19 LLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTE 78
                                                                                                                                                                                                       DSRFRELRKRYEDLLTRLRANQ-----SWEDSNTDLVPAPAVRILTPEVRLGSGG--
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                                                      ----ARPQAPALHLRL--SPPPSQSDQLLAESSSARPQLELHLRPQAARGRRRARARNG
                                                                                         LPGRFVAESAEVLLPRLVSCPGPLDQDQ-----
                                                                                                                               HLHLRISRA---ALPEGLPEASRLHRALFRLSPTASRSWDVTRPLRRQLSL------
                                                                                                                                                                  RFFSRITKANVDLLPRGAPERQ-----RLLPAALACWGVRGSLLSEADVRALGGLACD 189
                                                                                                                                                                                                                                          --RVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACT 136
                                                                                                                                                                                                                                                                                 MLLVLLVLSWL------PHGGAL-----SLAEASRASFP--GPSELHTE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QGLLRVRWLRLSHNALSVLAPEALAGLPALRRLSLHHNELQALPGPVLSQARGLARLEL
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                                                                                                                                                                                                                                                                                                                                                                             Score 96.5; DB 5; Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                           -QEAARA----ALQG 227
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                                                                                                                                                                                                                                                                                                                                                            137;
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                                                                                      RESULT 14
US-09-897-516-6629
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                                                    Sequence 6629, Application US/09897516 GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 188
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lasek, Amy W
APPLICANT: Jones, David
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Best Local Similarity
           APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry S.
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TYPE: PRT
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FILE REFERENCE: PA-0038 US
 APPLICANT:
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                                                                                                                                                                PASYNPM-VLIQKTD 289
                                                                                                                                                                                                                                                                                                                      DHCPLGPGRCCRLHTVRA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACT 136
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                                                                                                                                                                                                                                            SP---REVQVTMCIGACPSQFRAA----
                                                                                                                                                                                                                                                                                 RPRFRREVEKT----ACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNA----I 340
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Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 0.
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US-09-815-242-5107; Sequence 5107; A
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US-09-897-516-6629
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PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 6629
LENGTH: 689
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION
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Best Local Similarity
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                                TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILLING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Malvar, Thomas M.
APPLICANT: Slater, Steven C.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT EPPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
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                                                                                                                                                                           Xu, H. Howard
                                                                                                                                                                                                                                                       Wall, Daniel
                                                                                                                                                                                                                  Trawick, John D. Carr, Grant J.
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Zyskind, Judith W.
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION 1000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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Best Local Similarity 22.3
Matches 89; Conservative
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                                                                                                                                                                                                                  418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 SRDPS-----WRQP---ERTILRPRF-----RREVEKTACPSGKKAREID 310
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                                                                                                                                                                       DGVPVQRVHGDGGLHMDWQD-----FSALDRDSRQQHLQTLADSE--AHRPFDLES----
                                                                                                                                                                                                               ATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPR 477
                                                                                                                                                                                                                                                             W-QLEPDSPAYNVGGLARLSGPLDVARFEA----ALQALVQ---RHE----TLRTTFPSV
                                                                                                                                                                                                                                                                                                     YPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLPQV 417
                                                                                                                                                                                                                                                                                                                                                LPLRALFEASELEAFCEQVRAAQAAGRTDSHGAIRRIDREQPVPLSYSQ-----QRMWFL
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FLDDRESPLEPLPVQYLDYSVWQR-EWLESGERQRQLDYW 1922
                                      FMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDW 568
                                                                                     ----GPLLRVCMVKMAEREHYLVV---
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Pred. No. 4:
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21;

Search completed: December 7, 2001, 09:49:36
Job time: 94 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model
Run on: December 7, 2001, 09:52:27; Search time 33.02 Seconds
(without alignments)
1448.747 Million cell updates/sec
Title: US-09-215-035-2
Perfect score: 3261
Sequence: 1 MALQRLDPCWSCGDRPGSLL.....LLGPGPVLTVLALLLASTLA 628
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 .

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	. 16	15	14	13	12	11	10	9	8	7	თ	G	4	ω	N	ш	NO.	Result	
104.5	105	105	105	105	105	105	105.5	106	106	106	106	106.5	106.5	107.5	107.5	108	108.5	108.5	108.5	108.5	109	110	110.5	111.5	111.5	120	125.5	1708	Score		
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hypothetical prote	hypothetical prote	probable metallopr	ankyrin-like prote	conserved hypothet		hypothetical prote	hypothetical prote	exodeoxyribonuclea		probable fibronect	probable lipase -	integrin beta-4 ch	amyloid precursor-	U)	5-oxoprolinase (AT		hypothetical prote	hypothetical helic	Dna2p - fission ye		hypothetical prote	×	1	protein -			othetical p	Erc protein - rat	Description		

В

360 KTYPQGYPESLIKQLGHEFRYVSPEDIRQWNVTSPDTVNTLLKVSKGQKMD------A 411

45	44	43	42	41	40	39	38	37	36	35	34	υ W	32	31	30
101	101	101.5	101.5	102	102	102.5	102.5	102.5	102.5	103.5	103.5	103.5	104	104	104
3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3. ₁	3.2	3.2	3.2	3 .2	3.2	3.2
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virginiamycin S sy	nucleobindin - hum	still frameshift p	pilin biosynthetic	avrBs3-2 protein -	DNA-directed DNA p	probable ATP-depen	probable large ATP	cell division cont	hypothetical prote	protein kinase (EC	chemotaxis protein	hypothetical prote	FK506 polyketide s	glycinetRNA liga	hypothetical prote

ALIGNMENTS

	356 ELYPOGYPESVIOHLGYLFLKMSPEDIRKWNYTSLETLKALLEVDKGHEMSPQAPRRPLP 415	Qy	
	300 EQKACPPGKEPNVVDENLIFYQNWELEACVDGTLLAGQMDLVNEIPFTYEQLSIFKHKLD 359	Дb	
	296 EKTACPSGKKAREIDESLIFYKKWELEACVDAALLATOMDRVNAIPFTYEQLDVLKHKLD 355	Qy	
		рь	
	236 STWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREV 295	Qy	
	180 SETDARALGGLACDLPGEFVAKSSEVLLPWLARCGGPLDQGQAKAVREVLRSGRAPYGPP 239	Дb	
	176 SEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPP 235	Qy	
	120 LPLDLLLFLNPAMFPGQQACAHFFSLISKANVNVLPRRSLERQRLLTGALKCQGVYGFQV 179	Дb	
	116 LPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLL 175	Qy	
	60 SLPTGLFLGLTCDEVSGLSMGHAKELAMAVRQKNIVLQVHQLRCLARRLPKHLTNEELDA 119	DЬ	
	58 SLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDA 115	Оу	
	1 MALPTAQPLLGSCGSPICSRSFLLLLLSLGWLPLLQTQTTRTSQEAALLHAVTGTV-DFA 59	Db	
	1 MALQRLDP-CWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNIS 57	Qy	
5;	Query Match 52.4%; Score 1708; DB 2; Length 625; Best Local Similarity. 55.7%; Pred. No. 3.1e-114; Matches 351; Conservative 81; Mismatches 184; Indels 14; Gaps	Qu Be Ma	
	A; Map position: 10q12	A;Ge A;Ma	
involved in	umor marker for renal cell carcinoma, is	00;00 00;00	
	A;Residues 1-625 <yam> A;Residues 1-625 <yam> A:Cross references: DDBT:DR7351</yam></yam>	A; Re	
	A;Accession: JC7362 A:Molecule type: mRNA	A; Ac	
preferentiall		A;Ti A;Re	
	mashita, Y.; Yokoyama, M.; Kobayashi, E.; Takai, S.; Hino, O. hem. Biophys. Res. Commun. 275, 134–140, 2000	R;Ya	
	ETC PROTEIN - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000 C:Arcession: T77162	C; Da	
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A;Residues: 1-2109 <DOW>
A;Cross-references: EMBL:M83200; NID:g468913; PID:g468914; PIDN:AAA73173
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R;Downie, S.R.; Katz-Downie, D.S.; Wolfe, K.H.;
Curr. Genet. 25, 367-378, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Pelargonium x hortorum
C;Species: Pelargonium x hortorum
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31352
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Best Local Similarity
Matches 128; Conserv
     1412
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- - PTREDDEIEDQAEMDTRRDLDGIEYTHAIQDMI----
                                                                    PLITLEMEARSSWPFFQHLDEIYGDQLEYVYDDTSLSVEVEE----EEDTSWGIEEWSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCDPRQLDVLYPKARL-AFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMK
                                                                                                                                               YQTMTYSKTSCGVNAFHFPSHEKPFSFRLDLSPPRGILVIGSIGTGRSYLIKSLAKNTHF
                                                                                                                                                                                                                    VDQILLSLTQSSKNASGSQMIEQPGEMYLR-HVVDLQKKYLMGYEFNTSSLAERRIFLAH 1299
                                                                                                                                                                                                                                                            LDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRK------WNVTSLETLKALLE-
                                                                                                                                                                                                                                                                                                                               EKTACPSGKKAREIDESLIFYKKW---ELEACVDAALLATQMDRVNAIPF-----TYEQ
                                                                                                                                                                                                                                                                                                                                                                        SNWNLNLID-ISDLISLIPNPIDR-ITFSINTRHLSHTSKE----IYSFIRKRER---
                                                                                                                                                                                                                                                                                                                                                                                           STWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRPRRREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIREIS-RMCLRNLTLSAERIRRNNESPLTHTHLRSPNVLEFLYSTLLLLL....VAGYL 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVRELAVALAQKNVKLSTEQLR-----CLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLSVQETLSGTPCLLGPGPVLTVLALLLAS 625
                                                                                                                                                                                    -----VDKGHEMSPOAP---RRPL--PQVATLIDRFVKGRGQLDKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              EE-----LEGGGRAYGVEAIF 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTRFFSRITKANVDL-----LPRGAPERQRLL----PAALACWGVRGSLLSEA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DENVREAFSSGAPLLGPGEVEAWIPALLSA 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%; Score 125.5; [
20.5%; Pred. No. 2.2;
Live 91; Mismatches
                                                                                                                                                                                                                                                                                             -- VYGAWIDDKIESLLSTSVAIDDCDRGNLLQFSTLTLTTEKG
                                                                                                             -DTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLD
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   DL-----GISVDAQ--LN
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A;Residues: 1-2218 <STO>
A;Cross-references: GB:AE002093; NID:g4803953; PIDN:AAD29825.1; GSPDB:GN00139
C;Genetics:
C;Gene: At2g28300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: B84683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1506 MTPCILWIPNIHDV-DLEDRTTLAG
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                                             HEMSPQAPRRPLPQVATL-
                                                                                           VGE--PSATTRTNVPD-----AQSPGEM---NLHTVETHKAEDSSGLKNQEALYNLSKA
                                                                                                                                    LDELYPOGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLK-----ALLEVDKG
                                                                                                                                                                                                                               EVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHK
                                                                                                                                                                                                                                                                                                                                                                                                                     ALRGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RITKANVDLLPRGAPER-QRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPTSSLALTSPDLSGPPGFQSLP------ASPAPTPIRGRGRGRGRGRGRGRGRR
DKLVSDIP-HPVPGDLTTSGSVANKDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNT
                                                                                                                                                                                                                                                                                                                          SSRDPSWRQPER------RPRFRR
                                                                                                                                                                                                                                                                                                                                                                        ALQGVTTAPSDATLPMSSQPSDATLPMSSQPVGSTVEAQEANVPSLPAALPAKRRVRNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VQTLNVLENSSERKAFAVKKRPLIQGGGPVQNQNAVSSVCDGSKSPSEGRTYT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVLLPRLVSCPGPLDQDQQEAA-----RAALQGGGPPYGPPSTWSV-----STMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVPKAN-----EGSTSNPDQVSPVHSATTALRSDKAADKDL------DAPPGFDSGSH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGVLHGSNSSITQRTETATSLA-----SDAEA-----TKFALPRSASEIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAVALAQKNVKLS--TEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFS 140
                                                                                                                                                                                    SVAPDIHSSGSLSQEIRRDTSGTGGSARKQTADVTDVARVMKEI-----FSETSLLKHK
                                                                                                                                                                                                                                                                            SRGETPKRQGKRRGQPLPATDASSARSTGLTPQIEVKVGNLSGTKAKFDAVAKEQPHFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                   --LPVLGQPI-----IRSIPQGIVAAWRQR---
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VKGRGQLDKDTLDTL----

TAFYPGYLCSLSPEELSSV----

-PPSSIWAVR 467

CSLSPEELSSVPP 460 	TLIDRFVKGRQQLDKDTLDTLTAFYPGYL :	y 419 5 3989	p Q
ALLEVDKGHEMSPQAPRRPLPQVA 418	GYLFLKMSPEDIRKWNVTSLETLK	y 371 5 3934	DP Q
DELYPOGYPESVIQHL 370	SLIFYKKWELEACVDAALLATQMD-RVNAIPFTYEQLDVLKHKLDE : :: : : : : : :	y 312 5 3885	р 8
-KTACPSGKKARĖIDE 311 	IVAAWRQRSSRDPSWRQPERTILRPRFRREVE	265 3831	D Qy
VLGQPIIRSIPGG 264 	PGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLP	7 210 5 3775	дь 94
PRLVSC 209	2 GSLLSEADVRALGGLACDLPGRFVAESAEVLL	172 3723	₽ &
ERORLLPAALACWGVR 171 	4 DALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVR	114 3669	B 8
RCLAHRLSEPPEDL 113 	GFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLR	66 3615	B &
LTTPHNISSLSPRQLL 65	B PCWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISSLSPRQLL	3557	ρ δ
Length 4957; Indels 195; Gaps 34;	Query Match 3.4%; Score 111.5; DB 2; Le Best Local Similarity 19.9%; Pred. No. 74; Matches 148; Conservative 112; Mismatches 287; Ir	Query Ma Best Loc Matches	
ASSLSYVRSEPTASA 697 FIGGAPTEDLKALSQONVS 523	TAKSSIEKCTADQLLGEKLSQEGETTPASDĞETCHLAEET QDLDTCDPRQLDVLYPKARLAEQNMNGSEYFVKIQS	Db 642 L Oy 468 P Db 698 - Qy 524 M Db 742 S Db 742 S Db 742 S T03455 C;Species: C;Caccesion R;Prasad, R C;Accession R;Prasad, R Oncogene 15 A;Title: St A;Refectes: A;Refe	CCAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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ALR protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03454
R;Prasad, R; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yancession: T5, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, a novel gene with strong homo A;Reference number: Z14954; MUID:973884774
A;Accession: T03454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 12
C;Superfamily: human ALR protein
C;Keywords: alternative splicing
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C;Genetics:
A;Gene: ALR
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A; Residues: 1-5262 < PRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3862 PSVSLGDQPGSMTQNL--LGPQQPMLERPMQNNTGPQPPKPGPVLQSGQGLPGVGIMPTV 3919
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                                                     4190 KLLRAKNVQLSTGQGSEGLRAEINGHIDS-----KLAGLEQKL-----QGTPSNKEDAA 4238
                                                                                                                                                                                                                                                                                                                                                                                                4028 GPVHPTPPPSSPQEPKR-----PSQLPSPSSQLPTEAQLPPTHPGTPKPQGPTLEPP 4079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3920 GQLRAQLQGVLAKNPQLRHLSPQQQQQLQALLMQRQLQQSQ-----AVRQTPPYQEPGT 3973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4107 QTEDVRMESDEDSD------SPDSIVPASSPE--SILGEEAPREPHLGSGRWEQEDR 4155
                                                                                                                                                                        4136 SQLSIKQEPREEPC-----ALGAQSVKREANGEPIGAPGTSNHLLLAGPRSEAGHLLLQ 4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3974 QTSPLQGLLGCQPQLGGFPGPQT-----GPLQELGAGPRPQG-PPRLPAPPGALSTGPVL 4027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 GSL------LSEADVRALGGLACDLPGRFVAESAEVLL--------PRLVSC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 DALPLDLLLELNPD -- AFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVR 171
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371 GYLFLKMSPEDIRKWN---VTSLETLK-----
                                                                                                                                                                                                                             265 IVAAWRQRSSRDPSWRQPERTILRPRFRREVE------KTACPSGKKAREIDE 311
                                                                                                                                                                                                                                                                                                                                          210 PGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLP-----VLGQPIIRSIPQG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GFPCAEVSG-----LSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPED--L 113
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                                                                                                       SLIFYKKWELEACVDAALLATOMD-RVNAIPFTYEOLDVLKHKLDELYPOGYPESVIOHL 370
                                                                                                                                                                                                                                                                                  PGRVSPAAAQLADTLESKGLGPWDPPDNLAETQKPEQSSLVPGHLDQVNGQ----VVPEA 4135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCWSCGDRPGSLLFLLFSLGWVHP--ARTLAGETGTESAPLGGVLTTPHNISSLSPRQLL
-ALLEVDKGHEMSPQAPRRPLPQVA 418
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hypothetical protein F8A5.20 [imported] - Arabidopsis thaliana C;Specles: Arabidopsis thaliana (mouse-ear cress)
C;Specles: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #text_change 23-Mar-2001
C;Accession: B96632
C;Accession: B96632
C;Accession: B96632
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Reference number: A86141; MUID:21016719
A;Reference number: A86141; MUID:21016719
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A;Map position: 1
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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A; Residues: 1-340 <STO>
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Best Local
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PSWROPERT LRPRFRREVEKTACPSGKKAREIDESLIFYKK---
                                           RAHAVHPITAVQIEWSLWSRDAEEDIIPICRELGIGIVAYSPLGRGFLAAGPKLAENLEN
                                                                                                                             RAACEASLKRLDIACIDLYYQHRIDTRVPIEITMRELKKLVEEGKIKYIGLSEASASTIR
                                                                                                                                                                  AESAEVLLPRL-VSCPG-----PLDQDQQEAARAALQGG----GPPYGPPST--
                                                                                                                                                                                                             ---DTSDMYGPETNELLLGKALKDGVKEKVELATKFGFFIVEGEISEVRG----DPEYV
                                                                                                                                                                                                                                                      ANVDLLPRGAPERQRLLPAALACWGVR------GSLLSEADVRALGGLACDLPGRFV 195
                                                                                                                                                                                                                                                                                                  LGSQGLEVSAQGLGCMALSARYGAPKPETDAIAL-----LHHAINSG----VTFF-----
                                                                                                                                                                                                                                                                                                                                    LAQKNVKLSTEQLRCLA -- HRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITK 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TEDLKALSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLG-----PHVEGLKAEERHR 563
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                                                                                                                                                                                                                                                                                                                                                                                    89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                    -WSVSTMDALRGLLPV---LGQPIIRSIP--QGIVAAWRQ--RSSRD 276
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                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                               Score 110.5;
Pred. No. 2;
62; Mismatches
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    -WELEACVDAALLAT
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A; Residues: 1-1770 <POS>
A; Residues: 1-1770 <POS>
A; Cross-references: EMBL:U24657; NID:g1171127; PID:g1171128; A; Experimental source: strain DM504-15
C; Genetics:
A; Gene: safB
C; Superfamily: acetate--CoA ligase homology; acyl carrier pro C; Keywords: carrier protein
F; 72-577/Domain: acetate--CoA ligase homology <ACL>
F; 618-688/Domain: acetate--CoA ligase homology <ACP1>
F; 1222-1659/Domain: acetate--CoA ligase homology <ACP1>
F; 1678-1746/Domain: acyl carrier protein homology <ACP2>
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A;Title: Two multifunctional peptide synthetases
A;Reference number: 218967; MUID:97090395
A;Accession: T18551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Pospiech, A.; Bietenhader, J.; Schupp, Microbiology 142, 741-746, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       saframycin Mx1 synthetase B - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
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                                             KKWEL - - - - -
                                                                                                                                                                                                                                                      EAAGREARPVSAPTPGTGERLPVPPGQRALW
                                                                                                                                                                                                                                                                                                                                                              WVHHQGDDVCPIPGTTK----
    RPFDLGRGPLLRTHLFSRAAQEHVLLLS-----VHHIVVDFWSLAVLVDELRRLYEAGGDG
                                                                                  VQQVHAHVPASFLVVDASGD-----DEAALRRRLLREA
                                                                                                                                                                                                                                                                                             TKANVDLLPRGAP-----ERORLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAE
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                                                                                                                           IRSIPQGIVAAWR-QRSSRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFY 316
                                                                                                                                                                                                         SAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                  RAICLQGALD---VEALRRAFQS------LVTRHPALRATFPMVGEEP
                                         -----EACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --AKPES--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3,4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 110; D
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 22;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TLAGET---GTES 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1770;
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-FLHQLAPDSPGYTIA-

735

197

689 142 639 88 579

У----

774

257

864 364 808 Indels 142;

Gaps

22;

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SLETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----QMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IENLNQNIRALSVKLTPEEI----S 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - NVDHNKILFEKVSAMAEKKGCTPAQLALA
                                                                             PID:g1171128;
                                                                                                                                                                                                 and an
                                                                                                                                                                                                                                                                               #text_change
                                                                                                                                                                                                   O-methyltransferase
protein
                                                                             PIDN: AAC44128
                                                                                                                                                                                                                                                                                 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -RYMA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388
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C;Accession: T35548

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A;Molecule type: DNA
A;Residues: 1-1171 <SEE>
A;Cross-references: EMBL:AL096825; PIDN:CAB46976.1; GSPDB:GN00070; SCOEDB:SC6G3.04
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SC6G3.04 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             699
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  959
                                                                                                                                                                                         877
                                                                                                                                                                                                                                  292
                                                                                                                                                                                                                                                                                   817
                                                                                                                                                                                                                                                                                                                                                                                758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 RIGIRIDGELYALSRRGSPLIQGAAQAARVILDIDGSDLIGTRIAGWYDTATGPDGRRRL 641
                                                                                                                                                                                                                                                                                                                                                                                                                         217 QQEAARAALQG------GGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIP-----QG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    642 ERRLTGVLVAAGFLIESASTALGPLFERVETMSDRGFLDRLYALRGGFRALTPQG---RS 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ---LPLD------PDAFSGPQACTRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522 LDSVRRRHLPGTTETVRIRAARLAGLLLDAAVRLLPGLAGSDEPRDAVAVVTLAVRSAAD 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 RENHRRAAEAGRVTSARVVALLGAAARCALTDLLHDGLTEAERVLPGAAALPELLAALDL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 LORLKECGYGYAEPVEVTGAGEGSALTTRWRAAWTPSVAARLDLYGVRGYTAAQAADGTL 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LORL------DPCWSCGDRPGSLLFLLFSLGW---VHPARTLAGETGTESAPLG-GVL 50
                                                                                                                                                                                                                                                                                 EEADEESRETNEGGDGGEPEPGAGGTSEGSDDDRTGGAARSFPSVRHWAEDLRTLFGAET 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLD--QD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSRITKANV-----DLLPRGAPERQ 158
RRPGGPLDLPRTLRANLAHIRRREDGRVEVVPERPVFRTRTARRNDWRLILVVDVSASME 1016
                                           RRP-----LPQV--ATL--IDRFVKGRGQL--DKDTLDTLTAFYPGYLCSLSPEELSSVP 459
                                                                                            ----LTLARGMPEQRVASLRPL-VKRLVEELTKELATRLRPTLTGL--
                                                                                                                                      HKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLE-TLKALLEVDKGHEMSPQAP 410
                                                                                                                                                                                    RQEVLERAVADGRT-------DVIALLDPASVRPSVELLSAV------
                                                                                                                                                                                                                                RREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLK 351
                                                                                                                                                                                                                                                                                                                               SAPAPRTAPSGAEVPHGAGAPRLGPADRWRLLLGRDTAG-LPAALRPYARALDELFDREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVLAAVSDRLGDRPDLRLPAPAELVGRWAA-ADGEGLALLGELGLADLASAPAAKDAGAT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KNVKLSTEQLRCLAHRL------ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69; Mismatches 246; Indels 310;
                                                                                            -TTPRPT 958
                                                                                                                                                                                      911
                                                                                                                                                                                                                                                                                                                                                                             816
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C; Superfamily: probable DNA helicase MJ0104

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C;Accession: T39568
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Brown, submitted to the EMBL Data Library, March 1999
A;Reference number: Z21864
A;Accession: T39568
A; Map position: 2
A; Introns: 120/1; 1052/2; 1290/3
                                                                                                                                             A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical helicase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Nov-2000
C;Accession: T39568
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A; Residues: 1-1397 <KAN>
A; Cross-references: EMBL: AF144384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dna2p - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C;Accession: T5129
C;Accession: T5129
C;Accession: T5129
C;Accession: MacNeill
C;Acces
                                                                                                                                                                           A;Cross-references: EMBL:AL035637; PIDN:CAB38508.1; A;Experimental source: strain 972h-; cosmid c16D10
                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1398 < WOO>
                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Introns: 120/1; 1051/2; 1289/3
C;Superfamily: probable DNA helicase MJ0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z25356
A;Accession: T51Z92
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                        A; Gene: SPDB: SPBC16D10.04c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIPN----GYLVLDLSVQETLSGTPCLLGP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIASIRGTL-----MSSVLPDAPLIIRDMIIRLKPPKFCNSALIDPEFLKCLNEDQIT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTAFYPGYLCSLSPEELSSVPPSSIWAVR------PQDLDTC--DPRQLDVLYPKARL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKG--------RGQLDKDTLDT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEIDDRVFHYKFAFLNDNGYPRNFL-HSGFSVGERVFIS---DEHGHWSLAKGHIVHIQ 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REI-DESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLD--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSTIVRLGSPH-----KIHPLVKEFCLTEGTTFDDLASLKHFYEDPQIVACSSLGVYH 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -AEVOKLLGPHVEGLKAEERHRPVRDWILRQRQ--DDLDTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMD----LATFMKLRTDAVLPLTV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSCIEVRTRHRL--HIPWLKMPNFDFKKNQVFFGNYEDSKLSFIGSNHTRYRIDKDEFSS 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVKDEDLEFYKKWEKLLNGEERLLL -- LKRGDVLTFDTEELEAYGKTLYPLYITKEDIV 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALKKCHAAEHYSLILGMPGTGKTTTISSLIRSLLAKKKKILLTSFTHLAVDNILIKLKGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VLKHKLDELYPQGYPESVIQHLGY----LFLKMSPEDIRKWNVTS---LETL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.; Churcher,
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nes 83; Conserv
                                                                DSTIVRLGSPH-----KIHPLVKEFCLTEGTTFDDLASLKHFYEDPQIVACSSLGVYH 105:
                                                                                                                                                                                                                                  LTAFYPGYLCSLSPEELSSVPPSSIWAVR-----PQDLDTC--DPRQLDVLYPKARL 488
                                                                                                                                                                                                                                                                                                      ALKKCHAAEHYSLILGMPGTGKTTTISSLIRSLLAKKKKILLTSFTHLAVDNILIKLKGC
                                                                                                                                                                                                  GIASIRGTL-----MSSVLPDAPLIIRDMIIRLKPPKFCNSALIDPEFLKCLNEDQIT 939
                                                                                                                                                                                                                                                                      DSCIEVRTRHRL--HIPWLKMPNFDFKKNQVFFGNYEDSKLSFIGSNHTRYRIDKDEFSS
                                                                                                                                                                                                                                                                                                                                        CLEIDDRVFHYKFAFLNDNGYPRNFL-HSGFSVGERVFIS---DEHGHWSLAKGHIVHIQ 828
                                                                                                                                                                                                                                                                                                                                                                        -----VLKHKLDELYPQGYPESVIQHLGY-----LFIKMSPEDIRKWNVTS---LETL 393
                                                                                                -AEVQKLLGPHVEGLKAEERHRPVRDWILRQRQ--DDLDTL------GLGLQG
                                                                                                                                                               AFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMD----LATFMKLRTDAVLPLTV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 108.5;
Pred. No. 20;
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밁 Qy DЬ Ωy Ъ 20 A;Cross-references: EMBL:U70852; PIDN:AAB09135.1; GSPDB:GN00022; CESP:F45E4.A;Experimental source: strain Bristol N2; clone F45E4 A; Description: The sequence A; Reference number: Z20082 A; Accession: T25752 hypothetical protein F45E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25752 A;Map position: 4 A;Introns: 60/2; 111/2; 939/3; 977/2; 998/1; 1021/1; 1125/3; 1140/3; 1157/2; 1173/2; A; Gene: CESP:F45E4.4 C; Genetics A; Molecule type: DNA A; Residues: 1-2361 <WIL> A;Status: preliminary; translated from GB/EMBL/DDBJ submitted to the EMBL Data Library, September 1996 A; Description: The sequence of C. elegans cosmid F45E4 R; Wilson, Query Match Matches 1215 1102 PGSRMLKRPNFGFLSNIANDAINKAKEAGSQIQAAVPIKPSSSSSNIVNNNVFSSSKSST 103 58 16 PGSLLFLLFSLGWV----HPARTLAGETGTE---SAPL------GGVLTTPHNIS Local Similarity SSNIPAGMEDLSEAEREKIMSVMANAEMEMGARFPPPSSQIPTRSPSVMSSSIMSELPPG AHRLSEPPEDLDALPLDLLLFLNPDA-----FSGP--QACTRFFSRITKANVDLLPRG 153 SLGTSAPTKSIPSPQIGIP---MDGLSEEERRQIMSVMAAADFDDSVNNVKPSTSG----SLS-----PRQLLGFPCAEVSGLSTERVRELAVALAQ-----KNVKLSTEQLRCL 102 134; Conservative 114; Mismatches 3.3%; Score 108.5; 19.4%; Pred. No. 43; DB 2; 252; Indels 191; Length 2361; Gaps 1214 1161 1274 57 36;

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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: E82662

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-283 <SIM>
A;Cross references: GB:AE003987; GB:AE003849; NID:g9106634; PIDN:AAF84411.1; GSPDB:GN001

A;Cross references: GB:AE003987; GB:AE003849; NID:g9106634; PIDN:AAF84411.1; GSPDB:GN001

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Resinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

Chado, M.A.; Madeira, A.M.B., Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palnieri, D.A

Rodriques, V.; Rosa, A.J. de M; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Reference, mumber: A59298

A;Reference, mumber: A59298

A;Reference, number: A59298

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C; Date: 18-Aug-2000
C; Accession: E82662
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                                                                                                                                                     A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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5-oxoprolinase (ATP-hydrolyzing) (EC 3.5.2.9) - rat
N;Alternate names: pyroglutamase (ATP-hydrolyzing)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T42756
R;Ye, G.J; Breslow, E:; Meister, A.
J. Blol. Chem. 271, 32293-32300, 1996
A;Title: The antho acid sequence of rat kidney 5-oxo-L-prolinase determined by cD
A;Reference number: Z22263; MUID:97113037
A;Accession: T42756
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1288 <YEG>
A;Residues: 1-1288 <YEG>
A;Cross-references: EMBL:070825; NID:91732064; PID:91732065; PIDN:AAC52955.1
A;Experimental source: Strain Sprague-Dawley; kidney
C;Superfamily: hypothetical protein YKL215c
C;Keywords: homodimer; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    265 VLFMR-SDGGLAPMDAFSGSRAVLSGPAGGVVGYSATTYHLEGGQP--VIGF---DMGGT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 LLFLLFSLGWVHPARTLAGETGTESAPLGGVL---TTPHNISSLSPRQLLGFPCAEVSGL
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                                                ----GPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILR 288
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FLTNGPCPASQLSLEEVAMGEVRVANEAMCRPI - - - -
                                                                                                                                                                                                                                         -DLLLFLNPD---AFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSL
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                                                                                                                                                        LSEADVRALGGLACDLPGREVAESAEVILLPRLVSCPGPLDQDQQEAARAALQGGGPPY--
                                                                                                                                                                                                           RSGLFVVGPESAGAHPGP-ACYRKGGPVTVTDANLV-----LGRLLPASFPC-----
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Pred. No. 21;
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A;Description: catalyzes the construction of a polyketide chain, which is then c A;Pathway: erythromycin biosynthesis C;Superfamily: [acyl-carrier-protein] S-malonyltransferase homology; 3-oxoacyl-[cort-chain alcohol dehydrogenase homology cort-chain alcohol dehydrogenase homology cort-chain alcohol dehydrogenase homology cort-cykeywords: acyltransferase; antibiotic biosynthesis; carrier protein; coenzyme F;52-453/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology coANTI> F;561-843/Domain: [acyl-carrier-protein] S-malonyltransferase homology cANTI>
                                                                                                                                                                 A;Gene: eryA
A;Start codon: GTG
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
S23070
                                                                                                                                                                                                                                                              A; Experimental source: strain CA340
                                                                                                                                                                                                                                                                                                                                3479, DH, 3480-3572 <BEV2>
A;Cross-references: EMBL:X62569; NID:g46977; PIDN:CAA44448.1; PID:g581651
R;Caffrey, P.; Bevitt, D.J.; Staunton, J.; Leadlay, P.F.
FEBS Lett. 304, 225-228, 1992
A;Title: Identification of DEBS 1, DEBS 2 and DEBS 3, the multienzyme pol A;Reference number: S23103; MUID:92316235
A;Accession: S23205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: 6-Deoxyerythronolide-B
A; Reference number: S23070; MUII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Bevitt, D.J.; Cortes, J.; Haydock, S.F.; Eur. J. Biochem. 204, 39-49, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994
C;Accession: S23070; S22011; S23205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erythronolide synthase (EC 2.3.1.94) II - N;Alternate names: 6-deoxyerythronolide B C;Species: Saccharopolyspora erythraea
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                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 2-12,'XXX' <
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A;Residues: 1-3573 <BEV1>
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\;Residues: 1-18
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561-843/Domain:
                                                                                                                                                                                                                                           ;Genetics:
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acyl carrier protein homology <ACP2>
: phosphopantetheine (Ser) (covalent) #status predicted
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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Gapop 10.0 , Gapext 0.5
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3261
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  Length DB
  SPK_HUMAN
PRKD_MOUSE
DP3A_HAEIN
LGN_HUMAN
RAGI_ONCMY
NCB1_HUMAN
ITB4_RAT
SYFB_THETH
IP3L_HUMAN
IL6B_MOUSE
CYGD_HUMAN
CYGE_RAT
MP12_RAT
DP0Q_HUMAN
EVPL_MOUSE
SAV_SULAC
IL6B_RATF
CYGD_CANFA
                                                                                                                                  ERY2_SACER
APP1_MOUSE
HRPO_BURSO
PKN1_MYXXA
DPO1_THETH
SYG_CHLTR
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APP1_HUMAN
CYGE_MOUSE
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OPLA_RAT
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Q00560
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P16785 human cytom	Q14999 homo sapien			P98063 mus musculu						P25552 escherichia		

ALIGNMENTS

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; AAC503 oprotein 1 1 2 2 32 5 587 6 557 6 559 6 550 7	Swiss : Swiss : Bioinfo Brofit this st ires a nail to	J. Cancer 57:90-97(1994). FUNCTION: MAY PLAY A ROLE IN CELLULAR ADHESION FRACTIVE WITH ANTIBODY K1. REACTIVE WITH ANTIBODY K1. SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE SUBCELLULAR LOCATION: CANCER PATIENTS. TISSUE SPECIFICITY: EXPRESSED IN MESOTHELIAL COVARIAN CANCERS, AND SOME SQUAMOUS CELL CARCIN PTM: GLYCOSYLATED.	FROM N.A., 14200897; Pul Pastan I.; r cloning ar by the Kl ar	rcinoma; foliases; Pub foliases; Pub Pastan I.; r cloning of elium, mesot l. Acad. Sci		0 (Rel. 39, 0 (Rel. 39, 0 (Rel. 39, PRECURSOR	STANDARD;
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GPI-al OTENTI/ EMOVED ESOTHEI -LINKEI -LINKEI	OT entry is copyright. It is Swiss Institute of Bioinformat Bioinformatics Institute. The profit institutions as long this statement is not removed ires a license agreement (See all to license@isb-sib.ch).	IN CELLULAR ACHED TO THE CANCER PATIE SSSED IN MESO SQUAMOUS CE	, AND CHARACTERIZATION PubMed=8150545;; and expression of a c antibody from an ovar	2591; lelin, a diss, and over	Craniata; V Catarrhini;	uence otati IGEN)	PRT; 6
or. MATURE MATURE GLCNAC. GLCNAC. GLCNAC. GLCNAC.	he de la p	JLAR ADHESION. AN THE MEMBRANE BY. VIENTS. AESOTHELIAL CELLS CELL CARCINOMAS	DNA ian	differentiation varian cancers.	; Vertebrata; lni; Hominidae	update) on update)	528 AA.
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SEQUENCE
                                                                                                                                                 APPL_HUMAN STANDARD; PRT; 650 AA.
APPL_HUMAN STANDARD; PRT; 650 AA.
P51693; 000113;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP).
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-98088960; PubMed-9428684;

Paliga K., Peraus G., Kreger S., Duwrrwang U., Hesse L

Masters C.L., Beyreuther K., Weidemann A.;

"Human amyloid precursor-like protein 1--cDNA cloning,

expression in COS-7 cells and identification of soluble
                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                           Homo
                                                                                       NCBI_TaxID=9606
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                                                                                                                           sapiens (Human).
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69044 MW;
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; 2783ED229C3855FD CRC64;
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                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Similarity 19.1%;
Matches 130; Conservative 7
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CARBOHYD
CONFLICT
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DOMAIN
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DOMAIN
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Pfam; PF02177; A4_EXTRA; 1.
PRINTS; PR00203; AMYLOIDA4.
SMART; SM00006; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. Use ntitles requires a license agreement (See htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lenkkeri U., Kestila M., Lamerdin J., McCready P., Olsen A., Tryggvason K.;
"Structure of the human amyloid-precursor-like prot 19913.1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98180887; Lenktor: "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 104775;
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Eur. J. Biochem. 250:3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. C-TERMINALLY PROCESSED IN THE GOLGI COMPLEX AND IS THEN SECRETED. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, PARTIN THE CEREBRAL CORTEX POSTSYNAPPIC DENSITY.

PTM: N- AND O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE APP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genet. 102:192-196(1998)
                          PIIRSIPQGIVAAWRQRSSRDPSWRQP-ERTILRPRFRREVEKTACPSGKKAREIDESLI
                                                                                                  GGSRSGSCAHPHHQVV-PFRC-LPGEFVSEA--LLVPEGCRFLHQERMDQCESSTRRHQE
                                                                                                                           WGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLP-----
                                                                                                                                                                                                                       PSTRSWPPGSRVEGAEDEEEEESFPQPVDDYFVEPPQAEEEEETVPPPSSHTLAV-----
                                                 AQEACSSQGLILHGSGMLLPCGSDRFRGVEYVCCPPPGTPDPSGTA------VGD
                                                                         QQEAARA---ALQGGG---
                                                                                                                                                 DLRTGRWEPDPQRSRRCLRDPQRVLEYCRQMYPELQIARVE-----QATQAIPMERWC
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650
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                                                                                                                                                                             -PQA---
                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                     79;
                                                                                                                                                                                                                                                    Score 123; DB 1
Pred. No. 0.37;
79; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal.

POTENTIAL.

AMYLOID-LIKE PROTEIN 1

EXTRACELLULAR (POTENT)
                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

P -> A (IN REF. 2).

121A034B708C67CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
CLATHRIN-BINDING (POTENTIAL).
                                                                                                                                                                          -CTRFFSRITKANVDLLPRGAPERQRLLPAALAC
                                                                         -PPYGPPSTWSVSTMDALRGLLPVLGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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THE STATE OF THE S
                 EMBL; L41933; AAC
HSSP; Q02846; 1AW
MGD; MGI:105123;
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GUCYZE OR GUCAL
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYGE_MOUSE STANDARD; PRT; 1108 AA. P52785; P52785; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) GUANYLYL CYCLASE GC-E PRECURSOR (EC 4.6.1.2)
                                                                                                                                                                                                                                                                                                                                                                             Genomics 31:367-372(1996).

- CAPALYTIC ACTIVITY: GTP = 3,'5'-CYCLIC GMP + PYROPHOSPHATE.

- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

- PTM: THERE ARE 9 CONSERVED CYSTEINE RESIDUES IN SENSORY GUANYLATE.

- CYCLASES, 6 IN THE EXTRACELLULAR DOMAIN, WHICH MAY BE INVOLVED IN INTRA- OR INTERCHAIN DISULFIDE BONDS.
                                                                                                              modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  guanylyl cyclase receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang R.B., Fulle H.J., Garbers D.L.; "Chromosomal localization and genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96435433; PubMed=8838319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              retina.";
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                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 PROTEIN KINASE-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
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                                         L41933; AAC42081.1;
Q02846; 1AWL.
IPR001828;
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ANF_receptor
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Sciurognathi; Muridae;
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in olfactory sensory
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                                                                                                                                                        Usage
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PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00211; guanylate_cyc; 1. Pfam; PF00069; pkinase; 1. SMART; SM00044; CYCC; 1.
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Vision; Glycoprotein.
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InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF01094; ANF_receptor; 1.
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VLKVTDHGHGRLLEA-QRVLPEPPSAEDQLWTAPELLRDPSLERRGTLAGDVFSLAIIMQ
                            ALLEVDKGHEMSPQAPRRPLPQVAT-----LIDRFVKGRGQLDKDTL-----
                                                                                                                              WLKKFPGEHHMAIRPATKTAFSKLRELRHENVALYLGLFLAGTADSP--ATPGEGILAVV
                                                                                                                                                            LRPRFRREVEKTACPSGK----KAREI-DESLIFYKKWELEACVDAALLATQMDRVNAI-
                                                                                                                                                                                                                                                                                              YGP-PSTW---
                                                                                                                                                                                                                                                                                                                                                              LPGR----
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                                                                                                                                                                                            IILTLEDVTFLHPPGGSSRKVVQGSRSSLATRSASDIRSVPS--QPQESTNVGLYEGDWV
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GUANYLYL CYCLA
EXTRACELLULAR
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INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

M; A1CC9E1B1444C803 CRC64;
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PROTEIN KINASE-LIKE.
GUANYLATE CYCLASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21201183; PubMed-11278896; Fujiwara S., Takeo N., Otani Y., Parry D.A.D., Kunimatsu M., Lu R., Sasaki M., Matsuo N., Khaleduzzaman M., Yoshioka H.; "Epiplakin, a novel member of the plakin family originally identified as a 450-kDa human epidermal autoantigen: structure and tissue localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Pukaryota; Butheria; Primates; Catarrhini; Hominidae;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EPIPLAKIN (450 KDA EPIDERMAL ANTIGEN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOI. Chem. 276:13340-13347(2001).

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN LIVER, SWALL INTESTINE, COLON, SALIVARY GLANDS, STOMACH AND APPENDIX.

SIMILARITY: CONTAINS 65 PLECTIN REPEATS.

SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
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                              GPRG-EVPAVWLLDAGIITQETLEALAQGTQS---PAQVAEQPAVKACLWGTGCVAGVLL 1228
                                                        GGLACDLP-----GRFVAESAEVLLPRLYSCPGPLDQDQQEAARAALQGGGPPYG---
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Submitted (AUG-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermus aquaticus (subsp. caldophilus) Bacteria; Thermus/Deinococcus group; T
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                              MEDLINE=93285135; PubMed=8508785;
Park J.H., Kim J.S., Kwon S.-T., Lee D.-S.;
"Purification and characterization of Thermus caldophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPO1_THECA P80194;
                                                                                                                                                                                                                                                  polymerase.";
Eur. J. Biochem. 214:135-140(1993)
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PIR; S33287; S33287
                EMBL; U62584;
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                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                      SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
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35, Last sequence update)
37, Last annotation update)
THERMOSTABLE (EC 2.7.7.7) (
                                                                                   rmatics Institute. There are no restrictions on institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                           Park J.H.,
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the EMBL/GenBank/DDBJ
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SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01367; 5_3_exonuclea Pfam; PF00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003583;
InterPro; IPR003584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN 412
SEQUENCE 834 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P19821; 1TAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000513;
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                                                                                                                   567
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                                                                                                                                                                                                                                                                                                                                                                                                                                               226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDLLP---RGAPERQRLLPAALACWGVRGSLLSEAD---
                                                                                                                                               GRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVP-----PSSIWAVRPQDLD
                                                                                                                                                                                                                                                                 QMDRVNAIPFTYEQLDVLKHKL-DEL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DNLPGVKGIGEKTAL--KLLKEWGSLENLLKNLDRVKPENVREKIKAHLEDLRLSLELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAPTPEDF - - - - PRQLALIKELVDLLGFTRLEVPGYEADDV - - - - LATLAKNPEKEGYE
 YGMSAHRLS---
                           RTDAVLPLTVAEVQKLLGPHVEGLKAEERH----RPVRDWILRQRQDDLDTLGLGLQGGI
                                                          QIELRVLAHLSGDENLIRVFQEGKDIHTQTASWMFGVPPEAVDPLMRR
                                                                                    TCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKL
                                                                                                                                                                            ---HQ1
                                                                                                                                                                                                       IQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVK 426
                                                                                                                                                                                                                                                                                                HRNLLKRLQGEEKLLWLYHEVEKPLSRVLAHMEATGVRLDVAYLQALSLELAEEIRRLEE
                                                                                                                                                                                                                                                                                                                          RR-----EVEK--TACPSGKKAREIDESLIFYKKWELEACVDAALLAT
                                                                                                                                                                                                                                                                                                                                                         AVLASREGLDLVPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEDAA----HRALLSERL
                                                                                                                                                                                                                                                                                                                                                                                                                    ----PPEGAFVGFVLSRPEPMWAELKALAACRDGRVHRAADPLAGLKDLKEVRGLLAKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                               QGGGPPYG-----PPSTWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRCLAHRLSEPPEDLDALPLDLLLFLNPDAF-----SGPQACTRFFSRITKAN 146
                                                                                                                ------NQTATATGRLSSSDP-NLQNIPVRTPLGQRIRRAFVAEAGWALVALDYS
                                                                                                                                                                                                                                     EVFRLAGHPFNLNSRDQLERVLFDELRLPALGKTQKTGKRSTSAAVLEALREAHPIVEKI
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                                                                                                                                                                            ---RELTKLKNTYVDPLPSLVH----
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 -QELAIPYEEAVAFIERYFQSFPKVRAWIEKT--------LEEGR
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93798 MW;
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19.4%;
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                                                                                                                                                                                                                                                                                                                                                                                   PVLGQPII----RSIPQGIVAAWRQRSSRDPSWRQPERTILRPRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80;
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Pred. No. 4.
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A851FF3C3076348E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VSTMDALRGLL----
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                                                                                                                                                                                                                                          EMBL; AF075169; AF0.22222..., Helicase; DNA-binding; ATP-binding; DNP_BIND 95 962 ATP (BY NP_BIND 120 MISSING CONFLICT 120 120 MISSING CONFLICT 120 120 MISSING CONFLICT 120 120 MM: C841
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-20341310; PubMed-10880469;
Kang H.-Y., Choi E., Bae S.-H., Lee K.-H., Gim B.-S., Kim H.-D.,
Park C., MacNeill S.A., Seo Y.-S.;
"Genetic analyses of Schizosaccharomyces pombe dna2+ reveal that
dna2 plays an essential role in Okazaki fragment metabolism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
DNA REPLICATION HELICASE DNA2.
DNA2 OR SPBC16D10.04C.
                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (Some or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasion S.G., Forsburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA2_SCHPO
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                                        773
                                                                     349
                                                                                                    715
                                                                                                                                  307
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       394 KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELONGATION AND MATURATION.
SUBUNIT: INTERACTS WITH CDC1, CDC24 AND RAD2.
SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
                                     CLEIDDRVFHYKFAFLNDNGYPRNFL-HSGFSVGERVFIS---DEHGHWSLAKGHIVHIQ
                                                                   -----VLKHKLDELYPQGYPESVIQHLGY-----LFLKMSPEDIRKWNVTS----LETL
                                                                                                  REVKDEDLEFYKKWEKLLNQEERLLL--LKRGDVLTFDTEELEAYGKTLYPLYITKEDIV
                                                                                                                               REI-DESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLD------
                                                                                                                                                                                                                                                                                               AF144384; AAD38528.1; -. AL035637; CAB38508.1; -. AF075169; AAC39502.1; -.
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                                                                                                                                                                                                                                        1398
                                                                                                                                                              Conservative
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                                                                                                                                                                           3.3%;
                                                                                                                                                                                                                                     g; ATP-binding; DNA replication.
62 ATP (BY SIMILARITY).
20 MISSING (IN REF. 1).
157786 MW; C848F4378BAD9D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.L.;
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                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arrell B.G., Brown D., Churcl EMBL/GenBank/DDBJ databases
                                                                                                                                                                         Score 108.5;
Pred. No. 11;
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                                                                                                                                                             Mismatches
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                                                                                                                                                                                         DB 1;
                                                                                                                                                             140;
                                                                                                                                                                                         Length 1398;
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                                                                                                                                                             Indels
         -RGQLDKDTLDT
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RESULT 7
AUP1_H
AUP1_H
AC Q9Y679
DT 20-AUG
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AUP1_HUMAN STANDARD,
C9Y679; O9UNO6; O9Y685;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Novel genes expressed in hematopoietic stem/progenitor cells from myelodysplastic syndromes patient.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peng Y., Song H., Dai M., Huang Q., Mao Y., Zhang Q., ru
Luo M., Chen J., Hu R.;
"Human ancient ubiquitous protein AUP1 isoform gene.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gu J., Huang Q., Yu Y., Xu S., Han Z., Huang C., Ren S., Tu Y., Chen Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Hematopoietic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                                                                                                AF100754; AF100753;
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Shen Y., Chen Z.
                                                     ; AAD43018.1; -.; AAD43017.1; -.; AAF86645.1; -.; AAD43010.1; -.
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Best Local Similarity 22.6
Matches 114; Conservative
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P97608;
15-DEC-1998
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CONFLICT
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney; MEDLINE-97113037; PubMed-8942290; Ye G.-J., Breslow E., Meister A.; "The amino acid sequence of rat kidney 5-by cDNA cloning."; J. Biol. Chem. 271:32293-32300(1996).
                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
5-OXOPROLINASE (EC 3.5.2.9) (5-OXO-L-PROLINASE)
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1 37 PM
1 38 476 AM
1 160 165 PM
1 114 179 M
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Pred. No. 3;
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                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
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; Murinae; Rat
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ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ye G. J., Breslow E., Meister A.;
J. Biol. Chem. 272:4646-4646(1997).
-i- PUNCTION: CARALYZES THE CLEAVAGE OF 5-OXO-L-PROLINE TO FORM
GLUTAMATE COUPLED TO THE HYDROLYSIS OF ATP TO ADP AND INORGJ
PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; pF01968; Hydantoinase_A;
pfam; pF02538; Hydantoinase_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U70825; AAC52955.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002821; Hydantoinase_A.
InterPro; IPR003692; Hydantoinase_B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Sin
hes 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 LLFLLFSLGWVHPARTLAGETGTESAPLGGVL---TTPHNISSLSPRQLLGFPCAEVSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: WELL EXPRESSED IN TESTIS, K
SIMILARITY: BELONGS TO THE OXOPROLINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + 5-OXO-L-PROLINE + 2
PHOSPHATE + L-GLUTAMATE.
VEPGCQAEVTDTGDI-RISVGAEGPSMADTRLDPIQLSIF--
                                                              LQLE-DTPKIQTGPPHVEKVTQCYFEGGYQETPVYLLGELGYGHQLQGPCLIIDNNSTIL
                                                                                                                                                            SLSYTPETFAQLDQRLSRLEEQCVDALQVQGFPRSQISTESFLHLRYQGTDC
                                                                                                                                                                                                                          RVNAIPFTYEQLDVLKHKLDE-----LYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSL
                                                                                                                                                                                                                                                           ----AHVLACFGGAGGQHACAIARALGMDTVHIHRHSGLLSALGLALADVVHEAQEPC
                                                                                                                                                                                                                                                                                       PRFRREVEKTACPSG------KKAREIDESLIFYKKWELE----ACVDAALLATQMD
                                                                                                                                                                                                                                                                                                                         FLTNGPCPASQLSLEEVAMGFVRVANEAMCRPI ---- RALTQARGHDPS----
                                                                                                                                                                                                                                                                                                                                                          ----GPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STDVSRYAGEFEHVFEASTA----GVTLQAPQL------DINTVAAGGGSRLFF
                            ----CSLSPEELSSVPPSSIWAVRPQDLDT-CDPRQLDVLYPKARLAFQNMNGSEYFVKI
                                                                                              -QLDKDT
                                                                                                                             ----ALMVSAHQHPATACSPRAGDFGAAFVERYMREFGFIIPERPVVVDDVRVRGTGRSG
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Pred. No. 12;
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SHRFMSI
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_STANDARD; PRT; 3567 AA.

003132; 054096;
01-OCT-1993 (Rel. 27, Created)
01-OCT-1998 (Rel. 27, Last sequence update)
15-JUL-1998 (Rel. 36, Last anotation update)
ERYTHRONOLIDE SYNTHASE, MODULES 3 AND 4 (EC 2)
DEOXYERYTHRONOLIDE B SYNTHASE II) (DEBS 2).
                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                    EMBL; M63677; AAA26494.1;
EMBL; X62569; CAA44448.1;
HSSP; P28304; 1QOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91220065; PubMed-2024119;
Donadio S., Staver M.J., McAlpine J.B.,
"Modular organization of genes required biosynthesis.";
   InterPro;
                                                                                         or send
                                                                                                            entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bevitt D.J., Cortes J., Haydock S.F., Leadlay P.F.;
"6-Deoxyerythronolide-B synthase 2 from Saccharopolyspora
Cloning of the structural gene, sequence analysis and info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92155230; PubMed=1740151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
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NCBI_TaxID=1836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharopolyspora erythraea (Streptomyces erythraeus). Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Pseudonocardineae; Pseudonocardiaceae
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                                                                                                                                                                                                                                                           MISCELLANDOUS: BIOSYNTHESIS OF POLYKETIDES; ACYLTRANSFERASE (AT).
BETA-KETOACYL CARRIER PROTEIN SYNTHASE (KS), AND ACYL CARRIER
PROTEIN (ACP) FOR CHAIN ELONGATION. BETA-KETOREDUCTASE (KR),
DEHYDRATASE (DH), AND ENOYL REDUCTASE (ER) FOR PROCESSING OF THE
BETA CARBON, AND THIOSSTERASE (TE) FOR RELEASE AND LACTONIZATION
                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: IN EACH ORF OF ERYA TWO MODULES ARE PRESENT EACH ENCODING FOR A FUNCTIONAL SYNTHASE SUBUNIT. THUS ERYA SHOWING 3 ORFS CODES FOR 6 SYNTHASE SUBUNITS. IT IS SUPPOSED THAT EACH SYNTHASE PARTICIPATES IN ONE OF THE SIX FAS-LIKE ELONGATION STEPS REQUIRED FOR FORMATION OF THE POLYKETIDE. MODULE 1, 2, 3, 4, 5, AND 6 PARTICIPATING IN BIOSYNTHESIS STEPS 1, 2, 3, 4, 5, AND 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: 6 METHYLMALONYL-COA + PROPIONYL-COA =
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SIMILARITY:
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                                                                                        an email to license@isb-sib.ch).
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                                                                                                        requires a license agreement
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   IPR001227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the multifunctional enzyme.";
hem. 204:39-49(1992).
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   Acyltransf_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swanson S.J., Katz L.;
for complex polyketide
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                                                  KHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKA---
                                                                                                             KL--LDVVRGDGGPDPHERVDVL-QPVLFSIMVSLAELWRAHG----
                                                                                                                                 SVSTMDALRG-----
                                                                                                                                                      LVFPGQGAQWVGMARDLLESSEVFAESMSRCAEAL --
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                                                                                         FRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVL
                                                                                                                                                                        RALGGLACDLPG--RFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTW
                                                                                                                                                                                                                SGPQACTRFFSRITK-----ANVDLLPRGAPERQRLLPAALACWGVRGSLLSEADV
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IPR000794; Ketoacyl-synt.
IPR003880; Phosphopant_attach.
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                                                                                                                                                                                                                                                                                                                              3.3%;
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                                                                                                                                  -LLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPR
-KGHEMSPQ--APR--RPLPQVATLIDRFVKGRGQLDKDTLDT: | | | | | | | | | |
                             -GMVSVGASRDE------LETVLARWDGRVAVAAVNGPG
                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                     WW; F
                                                                                                                                                                                                                                                                                                                                                                              R -> A (IN REF. 2).
T -> S (IN REF. 2).
L -> F (IN REF. 2).
G -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                              Score 107.5;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHOPANTETHEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP (KR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACYL-ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHOPANTETHEINE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA-KETOACYL REDUCTASE ACYL CARRIER (ACP) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEHYDRATASE/ENOYLREDUCTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BETA-KETOACYL SYNTHASE
ACYLTRANSFERASE (AT) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON-FUNCTIONAL
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BETA-KETOACYL RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACYL CARRIER (ACP) 1
                                                                                                                                                                                                                                                                             -- RRAGVSSFGVSG--TNAHVIVEEAP----
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                      EE6284F4738AA0C0 CRC64;
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SE (AT) 1.
                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REDUCTASE 1
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Q03157;
Q1-QCT-1993
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                    TRANSMEM
DOMAIN
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              DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993
01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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  CARBOHYD
                                        DOMAIN
                                                                                           CHAIN
                                                                                                                   Glycoprotein;
                                                                                                                           PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
                                                                                                                                                                     Pfam; PF02177; A4_EXTRA; 1...
PRINTS; PR00203; AMYLOIDA4.
                                                                                                                                                                                             MGD; MGI:88046; Aplp1.
InterPro; IPR001868; A4_APP.
                                                                                                                                                                                                                                    EMBL; L04538; AAA37247.1;
                                                                                                                                                                                                                                                                                                                                                                                                                     Proc
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                                                                                                                                                                                                                                                                                                                                                                                                                                            'Identification of a mouse brain cDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         579
                                                                                                                                                                                                                                                                                                                                                                                         the Alzheimer disease-associated amyloid beta protein precu
oc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MAY BE PROC
IN THE GOLGI COMPLEX; HOWEVER, IT IS NOT YET CLEAR WHETER
                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE APP FAMILY.
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                                                                                                                                                          SM00006;
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
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                                                                                                                   Transmembrane;
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                                                                                                                                                       A4_EXTRA; 1.
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Rodentia;
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                        AMYLOID-LIKE PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CLATHRIN-BINDING (POTENTIAL).
POLY-GLU.
N-LINKED
                                                                                                                  Signal
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 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                              precursor.
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    RESULT 11
HRPO_BURSO
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Best Local
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01-JUN-1994 (Rel. 2
20-AUG-2001 (Rel. 4
HYPERSENSITIVITY RE
MEDLINE-93302711; PubMed-8316211;
Gough C.L., Genin S., Lopes V., Boucher C.A.;
Gough C.L., Genin S., Lopes V., Boucher C.A.;
"Homology between the HrpO protein of Pseudomonas solanacearum and bacterial proteins implicated in a signal peptide-independent secretion mechanism.";
Mol. Gen. Genet. 239:378-392(1993).
Mol. Gen. Genet. 239:378-392(1993).
THE SECRETION OF A PROTEINACEOUS ELICITOR THE HYDERSENSITIVITY RESPONSE IN PLANTS (BY SIMILARITY).

THE HYDERSENSITIVITY RESPONSE IN PLANTS (BY SIMILARITY).
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                                                                                                                                         SEQUENCE FROM N.A. STRAIN=GMI1000;
                                                                                                                                                                                                                                     Burkholderia solanacearum
                                                                                                                                                                                                                                                                                                                             P35656;
                                                                                                                                                                                                                                                                                                                                           HRPO_BURSO
                                                                                                                                                                                     NCBI_TaxID=305;
                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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119; Conserv
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                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                        29, Created)
29, Last sequence update)
40, Last annotation updat
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                                                                                                                                                                                                                     beta
                                                                                                                                                                                                                                                                    SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72;
                                                                                                                                                                                                                                     (Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                        -- REALSGLLIMGAGGGSLIVLSLLL
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                    subdivision; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56516DC3EA40E4B0 CRC64;
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                                                                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                                                                                                                                                                                                             690
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                                                                                                                                                                                                                                     solanacearum).
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30-MAY-2000
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TRANSMEM
                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE PKN1 (EC 2.7.1.-).
  Myxococcus xanthus
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SIMILARITY: BELONGS TO THE FHIPEP (FLAGELLA/HR/INVASION PROTEINS EXPORT PORE) FAMILY.
                                                                                                                                                                                                                                                                                               VLPLTVAEVQKLLGPHVEGL 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMRAIL-----ESLVVWGPKEKDTLMLVEYVRGDLGRQIAHQA-----
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                                                                                                                                                                                                                                                        ----RYVRRMIEPHLQAL 668
                                                                                                                                                                                                                                                                                                                                                                                RQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTDA
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PS00994; FHIPEP; 1.
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73990 MW;
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19.2%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation.
DOMAIN 59.
NP_BIND 65
NP_BIND 88
ACT_SITE 180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Munoz-Dorado J., Inouye S., Inouye M.;
"A gene encoding a protein serine/threonine kinase is required for normal development of M. xanthus, a gram-negative bacterium.";
Cell 67:995-1006(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as ins content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A41090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M73498; AAA25402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fransferase;
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InterPro; IPR001440; TPR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: PLAYS AN ESSENTIAL ROLE IN PROPER TIMING OF EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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  374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED TO START IMMEDIATELY BEFORE SPORE FORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                QRRLAPAAPAV -- PRASLVEVPVQVVLRPGESPVRLRGSGLS---RGGLFLHGGRVLPPL 432
                                                                                  LLATQMDRVNAIPFTYEQLDVLKHKLDELYPQ--GYPESVIQHLGYL--
                                                                                                                                                                                                                                                                                             CSRLPVVLELASGPLSV-MCEVVRVVPPAQARVWGMPTGFGVQFVEATAVLKAAVDALLQ 491
  --FLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSP
                                                                                                                            ESLEQHSLTPPQRAQVDALRV----RVREAAEALGATVQRALYDAWRGNHRGVAKCLEAG
                                                                                                                                                                     -QPERTILRPRFRREVEKTACPSGKKAREIDESL-----IFYKKWE-----LEACVDAA
                                                                                                                                                                                                            GEP-VRAVPQVPLTEDPAVARLLEAWRQRSAGDAYAVLALEPDSDMGTVRLRTREAWRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine/threonine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 F
73 A
88 A
180 B
88 K
74173 MW;
                                         -TAEQLESLRREFLARRPQAMGTARSHFQSGGALERDGQLSQALDQY
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
K-N: LOSS OF ATP-BINDING.
W; ED532EABF7215A91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
  407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPO1_THETH P52028; 01-OCT-1996
                                                                                                                                                                                                                      PRINTS; PRO0868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
PROSITE; PS00447; DNA_POLYMERASE_A;
                                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA polymerase gene (polA) from Thermus thermophilus J. Ferment. Bioeng. 76:265-269(1993).
-I- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHAT
                                                                                                                                                                                                                                                                                      Pfam; PF01367; 5_3_exonuclea Pfam; PF00476; DNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; D28878; BAA06033.1; -. HSSP; P19821; 1TAU.
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STRAIN-HB8 / ATCC 27634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermus aquaticus (subsp. thermophilus).
Bacteria; Thermus/Deinococcus group; Thermus
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15-DEC-1998
                                                                                                                                                                                                 DNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Urabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA POLYMERASE
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                            Transferase; DNA-directed DNA polymerase; DNA replication;
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                                                                                  GRAPTPEDF----PRQLALIKELVDLLGFTRLEVPGYEAD---DVLATLAKKAEKEGYEV 137
                                                                                                       GVLTTPHNISSLSPRQ------LLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQ
                                                              LRCLAHRLSEPPEDLDALPLDLLLFLNPDAF - - - - - -
 -DNLPGVKGIGEKTAL--KLLKEWGSLENLLKNLDRVKPENVREKIKAHLEDLRLSLELS
                                                                                                                          tch 3.2%; al Similarity 19.3%; 142; Conservative 8
                                                                                                                                                                                                                                                                                                           IPR001098; DNA_pol_A.
IPR000513; Exo_N_I.
IPR003583; HHH_1.
IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                      IPR002421; 5_3_exonuclease.
IPR002298; DNA_pol1.
                                        -RILTADRDLYQLVSDRVAVLHPEGHLITPEWLWEKYGLRPEQWVDFRALVGDPS
                                                                                                                                                                               834 AA;
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(Rel. 34, Last sequence update)
(Rel. 37, Last annotation update)
THERMOSTABLE (EC 2.7.7.7) (
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Pred. No. 11;
%1; Mismatches
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1A98145DC11A54A9 CRC64;
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                                                                          STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.
Mitchell W.P., Olinger L., Tatusov
                                                                                                                                                                                                                              STRAIN-L2/434/BU;
MEDLING-95394831; PubMed-7665503;
MEDGAT E.A., Glese M.J., Yasin B., Pang M.
"The glycyl-tRNA synthetase of Chlamydia
J. Bacteriol. 177:5179-5185(1995).
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
"Genome sequence of an obligate intracellular pathogen Chlamydia trachomatis.";
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InterPro; IPR002310; AA_tRNA_ligase_II.
InterPro; IPR002310; tRNA_synt_2e.
InterPro; IPR002311; tRNA_synt_2f.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00179; AA_TRNA_LIGASE_II_1; FALSE_NEG
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
Aminoacyl-trNA synthetase; Protein biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U20547; AAA82982.1;
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540 RRAIIKQGLQNLTGDQIVAIAPEHLIDETVFLTEHPFVISAQFDPAFCSLPKELLIAEMI
                                                    321 LEACVDAALLATQMDRVNAIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
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SUBCELLULAR LOCATION: COTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                     VAAWRQRSSRDPSW--RQ-PERTILRPRFRREVE--KTACPSGKKAREIDESLIFYKKWE
                                                                                                                                                                                                                                                                                                                                                           APERQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVL---LPRLVSC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIGSEELPATFVPTGIQQLESLAKKLLADHGIAYKHLEVLGTP----RRLALC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETGTESAPLGGVLTTPHNISSLSPRQL----LGFPCAEVSGLSTERVRELAVALAQKNVK
                                                                                                                                                                                                                                                       --PGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRG--LLPVLGQPIIRSIPQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRG 153
                                                                                                     V----SSGNTSWGHRQLDNRQLTIPSSNMYVDTLRSAC
                                                                                                                                                                                                        REPOKMTWD ----
                                                                                                                                                                                                                                                                                                         ALDQ----PSAI--WRVR-----SINGTDYLFLVIPEE-RKETAAILVNELPQLIRSI
                                                                                                                                                                                                                                                                                                                                                                                                            ----IEGLSHVTIRPESEKKGPPLSLLFM--TDGSVSPQG-EQFFS---SHGLSISHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 21.4%;
30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYCYL-TRNA SYNTHETASE ALPHA CHAIN.
GLYCYL-TRNA SYNTHETASE BETA CHAIN.
T -> A (IN SEROVAR L2).
D -> G (IN SEROVAR L2).
S -> P (IN SEROVAR L2).
S -> P (IN SEROVAR L2).
W -> C (IN SEROVAR L2).
I -> V (IN SEROVAR L2).
T -> P (IN SEROVAR L2).
T -> P (IN SEROVAR L2).
O -> I (IN SEROVAR L2).
ORSTPTONMOGETINRF -> PTVLPNTKYARRNHOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 104; I
Pred. No. 15;
                                                    ----FTYEQLDVLKHKLDELYPQGYPE----SVI 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> SARFAS. (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79EB918FE19D39E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TH (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221; Indels 184;
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                                                                                                   --VIVSQKE
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RESULT 15
SPK_HUMAN
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092797; 000733; 000689;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPK.

SPK.

Homo sapiens (Human).

'harvota; Metazoa; Chordata; 'harvota; harta; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Colon carcinoma;
MEDLINE-96354916; PubMed-8769423;
Keon B.H., Schaefer S., Kuhn C., Grund C.,
"Symplekin, a novel type of tight junction
J. Cell Biol. 134:1003-1018(1996).
                                                              between the Swiss Institute of Bioinfi
the European Bioinformatics Institute.
                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                               Alwazzan M., Hamshere M.G., I
"Six transcripts map within :
expanded repeat.";
Mamm. Genome 9:485-487(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYMPLEKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98252805; PubMed=9585442;
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                                                                                                                                                                                                                                                                                             FUNCTION: SPECIFIC COMPONENT OF TH
BUT MIGHT NOT BE AN EXCLUSIVELY JU
HOUSE-KEEPING RULE.
SUBCELLULAR LOCATION: CYTOPLASMIC
AND NUCLEOPLASM (MINOR) (IN CELLS
                                                                                                                           EPIDERMIS, INTERCALATED DISKS, PUI
AND LYMPH NODE.
MISCELLANEOUS: COULD BE USED AS A
DIFFERENTIAL DIAGNOSIS OF TUMORS.
                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: IN TESTIS, EXPRESSED IN POLAR EPITHELIA AND SERTOLI CELLS BUT NOT IN VASCULAR ENDOTHELIA. THE PROTEIN IS
                                                                                                                                                                               DETECTED IN STOMACH, DUODENUM, PANCREAS, LIVER, FETAL BRAIN, CARCINOMAS, LENS-FORMING CELLS, FIBROBLASTS, LYMPHOCYTES, LYMPHOMA CELLS, ENTHHROLEUKEMIA CELLS BUT NOT IN ENDOTHELIUM OF VESSELS, EPIDERMIS, INTERCALATED DISKS, PURKINJE FIBER CELLS OF THE HEART
                                                                                                                                                                                                                                                                                   WITHOUT TJ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ODDLDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAALAIGEHLQHITLGSSISTTGALLSILDRIDNLLSCFILGLLPTSSHDP---YALRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKEDIDTA ----- IHYCKADLVSSVVN---EFPELQGIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --QDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHQRYF----PTQNMQGEITN----RELIVCDNSPTDSIVEGNEKA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATFM------KLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQR 573
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                                                                                                                                                                                                                                                                                                                                                                    COMPONENT OF
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200 kilobases of the myotonic dystrophy
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                                                                                                                                                                                                                                                                                                                                                   THE TIGHT JUNCTION (TJ) PLAQUE, JUNCTIONAL COMPONENT. MAY HAVE
                                                                                                                                               A DIFFERENTIATION MARKER
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WITH
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plaque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U49240; AAC50667.1; -.
EMBL; V10931; CAA71861.1; -.
MIM; 602388; -
Cell adhesion; Tight junction; Nuclear protein.
DOMAIN 213 228 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DOMAIN 709 712 POLY-LEU
DOMAIN 1036 1043 POLY-SER.
SEQUENCE 1142 AA; 126499 MW; 46FFIB4C561C4409 GRC64;
                                                                                                                                                                                                                                                       408 QAPRRPL----PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSI 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 SSMSPLEEEAPQAKRRPEPIIPVTQPRLAGAGGRKKIFRLSDVLKPLTDAQVEAMKLGAV 434
                                524 MDLATFMKLRTDAVLPLTVAEV-QKLLG-PHVEGLKA 558
                                                                                                      741 LVKRVRDL-----YHKRLPDVRFLIPVLNG--
                                                                                                                                                   464 WAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVS 523
                                                                                                                                                                                                      696 EQPIRGMGMNSPELLLLVENCPKGAETLVTRCLHSLT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                596 VRSQALLFIKRMYEKEQLREYVEKFALNYLQLLVHPNPPSVLFGADKDTEVAAPWT---- 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 EIDESLIF----YKKWELEACVD-------AALLATQMDRVNAIPFTYEQL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                541 LITESALEVVRKYCEDESRTYLGMSTLRDLIFKRPSR-----QFQYLHVLLDLSSHEKDK 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 LYQEYNAYLAAGASGSLDKY------EDCLIRLLSGLQEKPDQKDGIFTKVVLEAP 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 KRILRÁEKAVACSGAAQVRIKILASLVTQFNSGLKAEVLS-FILEDVRA---RLDLAFAW 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 ERQRLLPAALACWG---VRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGP 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 ISGOSDTDITAEFLOPLLTPDNVANLVLISMVYLPEAMPASFQAIYTPVESAGTEAQIKH 316
773 QALPKLIKLN-----PIVVKEVFNRLLGTQHGEGNSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 LDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLP-------VLGQP 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LAGETGTE-SAPLGGVLTTPHNISSLSPRQLLGFPCA-----EVSGLSTE-RVRE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIRSIPQGIVAAWRQRSS------RDPSWRQPERTILRPRFRREVEKTACPSGKKAR 307
                                                                                                                                                                                                                                                                                                            ------EETVKQCLYLYLALLPQNHKLIHELAAVYTEAIADIKRTVLRVI 695
  804
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Search completed: December 7, 2001, 09:48:50 Job time: 53 sec

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Result
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Listing first 45 summaries
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1: sp_archea:*
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5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Match
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Gapop 10.0 , Gapext 0.5
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3261
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  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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sp_unclassified:*
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                                                                                                                                                                                                                                   Length
 630
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21313
1423
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10
                                   Q9WXJ0
Q32836
Q15029
Q9P0A9
Q9SL26
Q9AUB4
Q9U5Y1
Q75033
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Q14859
Q9BTR2
                                                                                                                           Q9ERA7
Q61468
Q9UK57
Q9F1J5
Q9UGS3
            Q9W5A4
Q9L8H4
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                                                                                                                                                                                                                                                                      SUMMARIES
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1643.568 Million cell updates/sec
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         Q9ugs3 homo sapien
Q9wxj0 corynebacte
Q3wxj0 corynebacte
Q3wx386 pelargonium
Q15029 homo sapien
Q9p0a9 homo sapien
Q9p0a9 arabidopsis
Q9aub4 arabidopsis
Q9aub4 arabidopsis
Q9u5y1 dictyosteli
Q7503 homo sapien
Q9w5a4 drosophila
Q918h4 streptomyce
                                                                                                                                                            Q9br17 homo sapien
Q14859 homo sapien
Q9btr2 homo sapien
Q9era7 rattus norv
Q61468 mus musculu
                                                                                                                                         Q9uk57
Q9f1j5
                                                                                                                                                                                                                                 Description
                                                                                                                                       homo sapien
pseudomonas
 caulobacter
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
106	106	107	107	107.5	108	108	108.5	108.5	108.5	108.5	109	110	110	110.5	111	111	111	111.5	111.5	111.5	112.5	112.5	113.5	113.5	114
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527	391	1715	451	757	793	283	2361	1398	652	636	1171	1770	912	340	3926	3851	1596	5262	4957	613	1012	730	1012	817	1067
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Q9RWV6	Q9Z360	Q9GLM4	Q9A844	Q9AJN7	Q9H5Z2	Q9PD02	094226	Q9URU2	Q9HTA6	Q9D0C6	Q9XAH6	Q50857	Q9K3Y2	022706	Q9UPA5	043161	Q918E1	014686	014687	Q9W8X7	Q9UKV7	·Q9TUG2	095712	Q9NK99	Q9Y1T2
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29rwv6	Q9z360	Q9g1m4	29a844	29ajn7)9 հ5z2	29pd02	294226	Q9uru2	Q9hta6	29d0c	Q9xah6	Q50857	9k3y2	02270	Q9upa5	043161	2918e	014686	214687	Q9w8x7)9ukv7	շ9էսց2	095712	Q9nk99	29y1t2
	streptomyce	bos taurus	caulobacter	arthrobacte		xylella fas			pseudomonas	Q9d0c6 mus musculu			<pre>streptomyce</pre>	o	homo	. homo sapien	1 fug		-	porc					drosophila

ALIGNMENTS

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239 SVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKT 298	179 DVRALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTW 238	119 DLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGYRGSLLSEA 178 	59 LSPROLLGFPCAEVSGLSTERVRELAVALAOKNVKLSTEOLRCLAHRLSEPPEDLDALPL 118 	1 MALORLDP-CWSCGDRP-GSLLFILFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISS 58	Sc Pr 4;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Cobley V.; Co	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	Ol-JUN-2001 (TrEMBLrel. 17, Created) Ol-JUN-2001 (TrEMBLrel. 17, Last sequence update) Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update) C335H7.1 (MESOTHELIN). MSLN	ULT 1 117 09BR17 PRELIMINARY; PRT.; 630 AA.

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Best Local (
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Q14859;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 270:21984-21990(1995).
EMBL; D49441; BAA08419.1; -.
InterPro; IPR000585; Hemopexin.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
PRE-PRO-MEGAKARYOCYTE POTENTIATING FACTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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95.4%;
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Pred. No. 4.8e-226;
3; Mismatches 16;
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MEGAKARYOCYTE POTENTIATING
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Q9BTR2;
Q9BTR2;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUS-PANCREATIC ADENOCARCINOMA;
TISSUS-PANCREATIC ADENOCARCINOMA;
Strausberg R.;
Strausber
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pred. No. 4.3e-225;
4; Mismatches 15;
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01-MAR-2001
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamashita Y., Yokoyama M., Kobayashi E., Takai S., Hino O.;
"Mapping and determination of the cDNA sequence of the Erc of preferentially expressed in renal cell carcinoma in the Tsc: mutant (Eker) rat model.";
Biochem. Biophys. Res. Commun. 275:134-140(2000).
EMBL; D87351; BAB13512.1;
EMBL; D87351; BAB13512.1;
SEQUENCE 625 AA; 68852 MW; 343EF77ADF390CD2 CRC64;
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55.98;
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Pred. No. 8.2e-123;
80; Mismatches 184;
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Merrota; Metazoa; Chordata;
Merria; Rodentia;
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Mammalia; Eutheria;
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Yamaguchi N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLP: ||||||||:||: ||: ||:||:||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVIALVACYLRGGGKLDEDIVKALDNIPLSYLCDFSPQDLHAIPSSVMWLVGLHDLDKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQKACPPGKEPNVVDENLIFYQNWELEACVDGTLLAGQMDLVNEIPFTYEQLSIFKHKLD
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                       MALQRLDP-CWSCGDR--PGSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNIS
MALPTARPLLGSCGSPICSRSFLLLLLSLGWIPRLQTQTTKTSQEATLLHAV-NGAADFA
                                                                                                                                                                                                                                                                                             D86370;
                                                                                                                                                                                                                                                                                                                Chem. 270:21984-21990(1995)
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625 i
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                                                                                        Conservative
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                                                                                                                                                                                                                                                                                           BAA13077.1;
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                                                                                                                                                                                                                                                                      Msln.
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69423
                                                                                                         52.3%;
                                                                                                                                                                                                                                                                                                                                                               expression
                                                                                                                                                                                                    MW;
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                                                                                      ;08
                                                                                    Score 1707; DB 11;
Pred. No. 1.4e-122;
30; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                    POTENTIAL.
9A5E9C3222C6983F CRC64;
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Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                         Taniguchi Y.,
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                                                                                                                                                                                                                                                                                                                                                               megakaryocyte
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                                                                                                                                                                                                                                                                                                                                                                                                           Tamura M.,
                                                                                        Indels
                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                               potentiating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                         0chi
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Query Match
Best Local Similarity
Matches 297; Conserv
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Q9UK57;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MESOTHELIN/MEGAKARYOCYTE POTENTIATING FACTOR (FRAGMENT).
Homo sapiens (Human)
                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S./
EMBL; AF180951; AAF01409.1;
                                                                                                                                                                                                                                                                                family are detectable in sera from patients with over Natl. Acad. Sci. U.S.A. 19:11531-11536(1999).
                                                                                                                                                                                                                                                                                                                                                                   Scholler N., Fu N., Yang Y., Ye Z., Hellstroem I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                 interPro;
                                                                                                                                                                                                                                                                                                                                   Soluble member(s) of the mesothelin/megakaryocyte potentiating factor
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLP 415 : || || || || || || || || || || || 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLVGLSVAEVQKLLGPNIVDLKTEEDKSPVRDWLFRQHQKDLDRLGLGLQGGIPNGYLVL
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                                                                                                                                                                                                           PS00024; HEMOPEXIN;
                                                                                                                                                                                                                                   IPR000585; Hemopexin
                                                                                                                                 398
398 AA;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                 398
43811 MW;
                             46.8%;
97.1%;
Score 1526; DB 4;
Pred. No. 5.6e-109;
1; Mismatches 0;
                                                                                                                                                                                                           UNKNOWN_1
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                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                  Takikawa Y., Eo S., Adachi S., Kojima M.;
"Deduced hrpo genes from Burkholderia glumae and subsp. avenae.";
Subsp. avenae.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ da EMBL; AB053455; BAB20913.1;
InterPro; IPR001712; Bact_exp_FHIPEP.
Pfam; PF00771; FHIPEP; 1.
PRINTS; PR00949; TYPE3IMAPROT.
SEQUENCE. 698 AA; 75549 MW; 488BE407FCE559A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9F1J5
Q9F1J5;
Q1-MAR-2001 (TrEMBLrel. 16,
Q1-MAR-2001 (TrEMBLrel. 16,
Q1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-GM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE HRPO.
Pseudomonas glumae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUTATIVE HRPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=337;
                           370
 247
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                                                                             DRAWRRETLASMQRVGR-KTEVPPILPRAPQFACAVGVR--
                                                                                                      TRFFSRITKANVDLLPRGAPERQRLLPAA - - LAC - WGVRGSLLSEADVRALGGLACDLPG
                                                                                                                                                                                    GMSAGDAANRFSVLSVGDAMVSQIPSLLL----SVAAGVMITRVADERQA----KQRSLGD
                                                                                                                                                                                                           GETGTESAPLGGYLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLST
RGLLPVL---
                                                  RFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGG-GPPYGPPSTW-----SVSTMDAL
                                                                                                                                E----IGHQLGSSSRALFFAAVLLLAFAIVPGFPSLLFVLLAAALSFAGYRLSVRKPSSR
                                                                                                                                                        EQLRCLAHRLSEPPEDLDALPLDLLLF-LNPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDLSVQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDLSVQ 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVNKGHEMS------
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                         -AANVAMPTLDAA-----FEAERAALQEALGLPFPGITMWVHAPLPVATFEIL
                                                                                                                                                                                                                                        Conservative
-GQ--
                                                                                                                                                                                                                                                  4.1%;
23.5%;
-PIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta
                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                     Score 133; DB Pred. No. 0.11; 70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                        4B8BE407FCE559A3 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              698
                                                                                                                                                                                                                                                                                                                                                                                            M.; glumae and Acidovorax avenae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą
                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                      209;
                                                                                                                                                                                                                                                               Length 698
                                                                                                                                                        -AFSG-----PQAC
                                                                                                                                                                                                                                      Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group;
                                                                            --TGPSI--
                                                                                                                                                                                                                                     Gaps
                                                                                                       192
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                                                                                                                                         Matches
                                                                                                                                                    Query Match
Best Local Similarity
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Q9UGS3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ756G23.1 (NOVEL LEUCINE RICH PROTEIN) (FRAGMENT).
DJ756G23.1.
                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DJ756G23.1.
Homo sapiens (Human).
Homo sapiens (Human).
'Arvota; Metazoa; Chordata;
'Arvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL035681; CAB63072.1; -.
                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                   PRINTS; PR00019; LEURICHRPT SMART; SM00370; LRR; 8.
                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                     Pfam; PF00560; LRR; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                              InterPro; IPR003591; LRR_typ.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000483;
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000372;
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              123
                                      251
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                                                               72
                                                                                                                15
                                      RLSLHHNELQALPGPV-----LSQARGLARLELGHNPLTYAGEEDGLALPGLRELLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSMDLATEMKLRTDAVLP-LTVAEVQKLLGPHVE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTS-LETLKALLEVDKGHEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHDVPHLMVTMPPGKAMLPDLRLVPAEVAAA----SARSCWRWPRR-----RGRPPVDS
------FLNPDAFSGPQACTRFFSRITKAN-VDLLP-----RGAPERQRLLPAALAC-----
                                                              VSGLSTERVRELAVALAQKNVKLSTEQLRCLAH-RLSEPP-----EDLDALP--LDLLL 122
                                                                                                             RPGSL--LELLFSLGWVHPARTLAGETGTESAPLGGVLTTPHN-ISSLSPRQLLGFPCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIWAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DQLSHDAPGLVAEVQKVLPPQRIADVLRRLLEEQVSIRNVRSFMESLIAWGAKEKDMLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTPRLDRRARGAGQDAV----WRTEQIIAHRLVAPCGATATLFLGIQEVQWI-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACPS-GKKAREIDESLIFYKKWELE-----ACVDAALLATQMDRVNAIPFTYEQL 347
                                                                                       RPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVRWLRLSHNALSVLAPEALAGLPALR 250
                                                                                                                                         113;
                                                                                                                                                                                                                                                                                           PF01462; LRRNT; 1. PF01463; LRRCT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SMDIRRYVRRMIESRLGWLSVYSYQE-LGEHVE
                                                                                                                                                                                                                SM00369; LRR_TYP; 4.
R 797 797
                                                                                                                                                                                                                                          SM00082; LRRCT; 2.
SM00013; LRRNT; 2.
                                                                                                                                                                                                                                                                                                                                                          IPR001611;
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                      AA:
                                                                                                                                                  4.08;
                                                                                                                                                                                                      85614 MW;
                                                                                                                                                                                                                                                                                                                                                          LRR.
                                                                                                                                                                                                                                                                                                                                                                                    LRR_Nterm
                                                                                                                                                                                                                                                                                                                                                                       LRR_Cterm.
                                                                                                                                        45;
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                                                                                                                                                    Score 131.5; D
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                     8C3247883EAE59AD CRC64;
                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          797
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                                                                                                                                                              DB 4;
                                                                                                                                      181;
                                                                                                                                                                Length
                                                                                                                                        Indels
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                                                                                                                                                                 797;
                                                                                                                                        125;
                                                                                                                                      Gaps
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                                      302
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RESULT
Q9WXJ0
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Best Local S
Matches 137
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum (Brevibacterium flavum)
Bacteria; Firmicutes; Actinobacteria; Actinobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ODXWed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL; AB025424; BAA76717.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS: PRO0415; ACONITASE.
ProDom; PD000511; Aconitase; 1
PROSITE; PS00450; ACONITASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00330; aconitase; 2. Pfam; PF00694; Aconitase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACONITASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01244; ACONITASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001030; Aconitase
InterPro; IPR000573; Aconitase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P16276; 1B0J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Brevibacterium lactofermentum ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1718;
                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 RAVAGPRAPPRGPPRGPGEERAVAPCPRACVCVPESRHSSCEGCGLQAVPRGF-----
  232 YGPPSTW----SVSTMDALRGLL-----
                                                                                                                                                                                                            115 AL-PLDLLL--FLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 -----RFLQV-----PGAALRALPSLFSLHLQDNAVDRLAPG
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                                                                                                                                                                                                                                                                79 TPARVLMODFTGVPC -- VVDLAT -- MREAVAA -
                                                                                                                                                                                                                                                                                                               60 SPROLL----GFPCAEVSGLSTERVRELAVALAQKNVKLSTEOLRCLAHRLSEPPEDLD
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                                                   ----SFSNFRVVP-----PGTGIVHQVNI---
                                                                                                     GSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPP
                                                                                                                                                           PLNPAEVVIDHSVIVEAFGRPDALAK----NVEIEYERNEERYQFLR-----WGSE
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137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                                                                                                                                                                                                                                                                     76;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                           Score 126;
Pred. No. 0.
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C 13869 acn
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  -PVLGQPIIRSIPQGIVAAWRQRSSRD
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gene for Aconitase.";
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                                                                       Query Match
Best Local
                                                         Matches
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Q32836;
Q1-NOV-1996
Q1-NOV-1996
    1006
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                                                                                                                                          InterPro; IPR003959; A
Pfam; PF00004; AAA; 1
Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                            Chloroplast.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=94363755; PubMed=8082181;

MEDLINE=94363755; PubMed=8082181;

Downle S.R., Katz-Downle D.S., Wolfe K.H., Calle P.J., Palme:

"Structure and evolution of the largest chloroplast gene (ORI

"Internal plasticity and multiple gene loss during angiosperm
                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid Geraniales; Geraniaceae; Pelargonium.
                                                                                                                               SEQUENCE
                                                                                                                                                                                  Curr. Genet. 25:367-378(1994).
EMBL; M83200; AAA73173.1; -.
                                                                                                                                                                                                               evolution.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4031;
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RIREIS-RMCLRNLTLSAERIRRNNESPLTHTHLRSPNVLEFLYSTLLLLL----VAGYL 1060
                            RVRELAVALAQKNVKLSTEQLR-----CLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQ 133
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                                                                       Similarity
                                                                                                                           il protein; Chloroplast.
2109 AA; 245645 MW; 948980477223DE8C
                                                         Conservative
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                                                                      3.8%;
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                                                                      Score 125.5;
Pred. No. 2;
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                                                                                                                                                                                                                                    J., Palmer J.D.;
gene (ORF2280):
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                                                                                    2109;
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O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KIAA0312 (UPSTREAM REGULATORY ELEMENT BINDING PROTEIN 1) (FRAGMENT).
KIAA0312 OR UREB1.
                                                                                                                                                           Nagase T., Ishikawa K., Nakajima D., Ohara Tanaka A., Kotani H., Nomura N., Ohara Prediction of the coding sequences of The complete sequences of 100 new cDNA
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               015029
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                                          Kim J.W., Lee Y., Hong Y.M., Hong M., Choe I.S.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AB002310; BAA20771.1; -
EMBL; AF057569; AAC62492.1; -
                                                                                                 SEQUENCE OF 1599-1906 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1506 MTPCILWIPNIHDV-DLEDRTTLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1356
                                                                                                                                  DNA Res.
                                                                                                                                                   code
                                                                                                                                                                                                                       MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                       TISSUE=BRAIN;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
               Ptam;
                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLITLEMEARSSWPFFQHLDEIYGDQLEYVYDDTSLSVEVEE----EEDTSWGIEEWSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKTACPSGKKAREIDESLIFYKKW----ELEACVDAALLATQMDRVNAIPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREV
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                                                                                                                                                   for
                PF00632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DTREDDEIEDQAEMDTRRDLDGIEYTHAIQDMI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----IPNGYLVLDLSVQETLSG
                                                                                                                                  large proteins in vitro 4:141-150(1997).
PS50237; HECT;
                           IPR000569; HECT
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               HECT;
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                                                                                                                                                                                                          Seki N.,
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                                                                                                                                                                             human
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                                                                                                                                                                                                          Miyajima
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Best Local
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NON_TER
SEQUENCE
Pfam;
SMART;
        Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S "Human partial CDS from cd34+ stem cells."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ EMBL; AF161390; AAF28950.1; -
Pfam; PF00632; HECT; 1.
                                                                                                                                                                                         01-OCT-2000 (TremBLrel. 15, 01-OCT-2000 (TremBLrel. 15, 01-JUN-2001 (TremBLrel. 17,
                                                                                                                                                                                                                                                                                                      1472
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                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                 HSPC272
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                                                                                              TISSUE-BLOOD;
                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                     ----SSMHISSSLP-
                                                                                                                                                                                                                                                                                                                   LKALSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQ
                                                                                                                                                                                                                                                                                                                                                      PLTPATPSSL---
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119; Conserv
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 HECTC;
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Primates;
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Pred. No. 2.2;
9; Mismatches 213
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                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                         sequence update)
annotation update)
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                                                                      S.J.,
                                               databases
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                                                                      Z.Q.,
Chen
                                                                                                                                                         Euteleostomi;
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                                                                                Wang
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Best Local Similarity 19:9
Matches 119; Conservative
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OSSL26
OSSL26
OL-MAY-2000 (TREMBLrel 1
OL-MAY-2000 (TREMBLrel 1
OL-MAY-0000 (TREMBLrel 1
ATTGC28800 PROTEIN
ATTGC28300
STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.'
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat
Buell C.R., Ketchum K.A., Lee J.J., Gill
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill
Cronin L.A., Shen M., Vanaken S.E., Goodman H.M., Somerville C
                                                                                                                        Eukaryota; thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidaeurosids II; Brassicales; Brassicaceae; Arabidopsis NCBI_TaxID-3702;
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NON_TER
SEQUENCE
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                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      LKALSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECLKELEESHDQHAVLVLQPAVEAFFLVHATERESKPPVRDTRESQLAHIKDEPPPLSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RREESPMDVDQPSPSAQDTQSIASDGTPQGEKEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRPRFRREVEKTA-------CPSGKKAREIDESLIFYKKWELEACVDAALLATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALVAATAISTIVVAASTTVTTPTTATTTVSISPTTKGSKSPAKVSDGGSSSTDFKMVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELSSVPPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TG--RLGSSGLGSASSIQAAVRQLEAEADAIIQMVREGQRARRQQQAATSES-SQSEASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AENVVIVASQKRPLGGRELQLPSMSMLTSKTSTQKFFLRVLQVIIQLRDDTRRANKKAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ERPPELPLLSEQL----SLDEL-----
                                                                                                                                                                                                                                                                                                                                                                     -SSMHISSSLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50237; HECT; 1.
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                                                                                                                                                                                                                                     13,
                                                                                                                                                                                                                                                                                                                                                                                                                             -DP
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                                                                                                                                                                                                                                     Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.
                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                    --PDTQKF---
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                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                    -- LRFAETHRTVLNQILRQ
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                                                             Town C.D.,
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                                                                                                                                                                Rosidae;
      C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT
Q9AUB4
ID Q9
AC Q9
DT Q9
DT Q1
DT Q1
DT Q1
OC Q5
OC Q5
OC Q5
OC Q5
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Best Local Similarity
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                              O9AUB4 PRELIMINARY; PRT; 3574 A
O9AUB4;
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence
O1-JUN-2001 (TrEMBLrel. 17, Last annotatio
PUTATIVE CHROMATIN REMODELING PROTEIN SYD.
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EMBL; AC006202; AAD29825.1; -.
                                                    SPLAYED
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                                                                                                                                                                                                                       SKIETNSEELQASRTDEV - - -
                                                                                                                                                                                                                                                MDLAT----FMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRD
                                                                                                                                                                                                                                                                                                           PQDLDTCDPRQLDVLYPKARLAFQN----MNGSEYFVKIQSFLGGAPTEDLKALSQQNVS
                                                                                                                                                                                                                                                                                                                                          LTAKSSLEKCTADQLLGEKLSQEGETTPASDGETCHLAEETASSLSYVRSEPTASA----
                                                                                                                                                                                                                                                                                                                                                                        VKGRGQLDKDTLDTL------TAFYPGYLCSLSPEELSSV-----PPSSIWAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMSPQAPRRPLPQVATL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGE--PSATTRTNVPD-----AQSPGEM---NLHTVETHKAEDSSGLKNQEALYNLSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLK------ALLEVDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVAPDIHSSGSLSQEIRRDTSGTGGSARKQTADVTDVARVMKEI-----FSETSLLKHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRGETPKRQGKRRGQPLPATDASSARSTGLTPQIEVKVGNLSGTKAKFDAVAKEQPHFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALRGL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVLLPRLVSCPGPLDQDQQEAA-----RAALQGGGPPYGPPSTWSV-----STMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAVALAQKNVKLS--TEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFS
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                                                                                                                                                                                                                                                                                                                                                                                                     DKLVSDIP-HPVPGDLTTSGSVANKDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135;
                                                                                                                                                                                                                                                                               STTAEPLPTDKL--EKNISFQDEVKTLNGD----KREAIL----LSSEEQTNVN
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                                                                             (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 17, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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AA; 235758 MW;
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                                                                               on update)
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         Rosidae;
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RESULT
Q9U5Y1
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
DT 01

Q9U5Y1

PRELIMINARY;

PRT;

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Q9U5Y1; 01-MAY-2000 01-MAY-2000 01-JUN-2001

MICROTUBULE-ASSOCIATED PROTEIN CP224

(TrEMBLrel. 13, I) (TrEMBLrel. 13, II) (TrEMBLrel. 17, II)

Created)
Last sequence up

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Best Local
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"SPLAYED, a Putative Chromatin Remodeling Fact
"SPEDIATED, a Putative Chromatin Remodeling Fact
Reproductive Development in Arabidopsis.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AF247809; AAK31908.1; -.

SEQUENCE 3574 AA; 389826 MW; 0CA25C1FF1AB6
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                               514 LKALSQQNVSMDLAT----FMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
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LSSEEQTNVNSKIETNSEELQASRTDEV-----
                                                                                                                                                                                                                            --ALLEVDKGHEMSPQAPRRPLPQVATL-----
                                                                                                                                                                                                                                                                                                                                                                                        PAKRRVRNLPSRGETPKRQGKRRGQPLPATDASSARSTGLTPQIEVKVGNLSGTKAKFDA 1825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPTSSLALTSPDLSGPPGFQSLP------ASPAPTPIRGRGRGRSRGRGAGRGRR 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPARTLA-----GETGTESAPLGGYLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRE
                                                                                                                              SVIQLSLGNTLTAKSSEEKCTADQLLGEKLSQEGETTPASDGETCHLAEETASSLSYVRS
                                                                                                                                                                                            QEALYNLSKADKLVSDIP-HPVPGDLTTSGSVANKDVDIGSSKVAAENELVKIPGGDVDS
                                                                                                                                                                                                                                                           FSETSLLKHKVGE--PSATTRTNVPD-----AQSPGEM---NLHTVETHKAEDSSGLKN 1928
                                                                                                                                                                                                                                                                                        YEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLK-----
                                                                                                                                                                                                                                                                                                                           VAKEQPHFSQSVAPDIHSSGSLSQEIRRDTSGTGGSARKQTADVTDVARVMKEI-----
                                                                                                                                                                                                                                                                                                                                                          ----RPRFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFT
                                                                                                                                                                                                                                                                                                                                                                                                                        VAAWRQR---SSRDPSWRQPER-----TIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSPSEGRTYTALQGVTTAPSDATLPMSSQPSDATLPMSSQPVGSTVEAQEANVPSLPAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----STMDALRGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSSERKAFAVKKRPLIQGVSSQHPGPNKQPLDLPVSTSSTLLGGGPVQNQNAVSSVCDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVPKAN-----EGSTSNPDQVSPVHSATTALRSDKAADKDLDAPPGFDSGSHVQTLNVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RITKANVDLLPRGAPER-QRLLPAALACWGVRGSLLSEAD------VRALGGLA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGVLHGSNSSITQRTETATSLA------SDAEA-----TKFALPRSASEIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVALAQKNVKLS--TEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFS 140
                                                                                             -PPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFQN----MNGSEYFVKIQSFLGGAPTED
                                                                                                                                                            ----IDRFVKGRGQLDKDTLDTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDLPGREVAESAEVLLPRLVS-CPGPLDQ--DQQEAARAALQGGGPPYGPPSTWSV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                               -STTAEPLPTDKL--EKNISFQDEVKTLNGD--
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Pred.
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No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LPVLGQPI-----
                                                                                                                                                              -TAFYPGYLCSLSPEELSSV-----
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-PHVDGKSVDVANQTVKE
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Best Local Similarity 23.3%; Pred. No. 9.2;
Matches 66; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graef R., Daunderer C., Schliwa M.;

"Dictyostellum DGCP224 is a microtubule-associated protein and a permanent centrosomal resident involved in centrosome duplication.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ012088; CAB56504.1; -.

InterPro; IPR000357; HEAT_repeat.

PROSITE: PS50077; HEAT_REPEAT; 1.

SEQUENCE 2015 AA; 224038 MW; BA64E982ADDC92EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID-44689;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-AX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                    216 DQ-----FEKLPTDPAVPLKYTRSEAAKALANASKGIQAK 250
                                                                                                                    519 QQNVSMDLATFMKLRTDAVLPL--TVAEVQKLLGPHVEGLKAE 559
                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                              477 RQLDVLYPKARLA--FQNMN-----GSEYFVKIQSFLGGA------PTEDLKALS 518
                                                                                                                                                                                                                                                                       448
                                                                                                                                                                                                                                                                                                                            394 -KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLTDTLTAFYPGYL-----
                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                       52 FKKILA-----DINPMSQERALEPLSAFIDRC------DCVNKFAASYVGVLVEKLF 97
                                                                                                                                                                                                                                                                                                                                                                                w
                                                                                                                                                          KQIPVKLILKQFSPWFENRDKGIRDQASELFIEIYRWIGKALIPLISEALTPIQ-LKALQ 215
                                                                                                                                                                                                                                 ASTRPRAKEKTIECLLLTIEADSAEPVVEALLKGTSSTSPKILLASL-AALTQALKTFGP 156
                                                                                                                                                                                                                                                                                                                                                                         DEEAPSGSIEDRINHKNW------KWRVSGLEELTTKERNSIEGSGPLENEWGPO 51
                                                                                                                                                                                                                                                                     -----SSIWAVRPQDLDTCDP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2015;
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